

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 17:17:11 ; Search time 685.5 Seconds
(without alignments)
1770.394 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28
Sequence: 1 cccatctcctcannatccctgtgttg 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_hgt:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
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- 11: gb_sta:*
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- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
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- 21: em_or:*
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- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sta:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_higo_hum:*
- 40: em_higo_mus:*
- 41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	25	89.3	2319	14	S66064	S66064 structural
C 2	25	89.3	2325	14	AF469175	AF469175 Dengue v1
C 3	25	89.3	2325	14	AF469176	AF469176 Dengue v1
C 4	25	89.3	2357	6	AR232496	AR232496 Sequence
C 5	25	89.3	2357	14	DEN2NGC	DEN2NGC Dengue viru
C 6	25	89.3	2552	14	AY152036S1	AY152036 Dengue v1
C 7	25	89.3	2552	14	AY152040S1	AY152040 Dengue v1
C 8	25	89.3	2552	14	AY152044S1	AY152044 Dengue v1
C 9	25	89.3	2552	14	AY152048S1	AY152048 Dengue v1
C 10	25	89.3	2552	14	AY152052S1	AY152052 Dengue v1
C 11	25	89.3	2552	14	AY152056S1	AY152056 Dengue v1
C 12	25	89.3	2552	14	AY152060S1	AY152060 Dengue v1
C 13	25	89.3	2552	14	AY152064S1	AY152064 Dengue v1
C 14	25	89.3	2552	14	AY152068S1	AY152068 Dengue v1
C 15	25	89.3	2552	14	AY152072S1	AY152072 Dengue v1
C 16	25	89.3	2552	14	AY152076S1	AY152076 Dengue v1
C 17	25	89.3	2552	14	AY152080S1	AY152080 Dengue v1
C 18	25	89.3	2552	14	AY152084S1	AY152084 Dengue v1
C 19	25	89.3	2552	14	AY152088S1	AY152088 Dengue v1
C 20	25	89.3	2552	14	AY152092S1	AY152092 Dengue v1
C 21	25	89.3	2552	14	AY152100S1	AY152100 Dengue v1
C 22	25	89.3	2552	14	AY152104S1	AY152104 Dengue v1
C 23	25	89.3	2552	14	AY152108S1	AY152108 Dengue v1
C 24	25	89.3	2552	14	AY152112S1	AY152112 Dengue v1
C 25	25	89.3	2552	14	AY152116S1	AY152116 Dengue v1
C 26	25	89.3	2552	14	AY152120S1	AY152120 Dengue v1
C 27	25	89.3	2552	14	AY152124S1	AY152124 Dengue v1
C 28	25	89.3	2552	14	AY152128S1	AY152128 Dengue v1
C 29	25	89.3	2552	14	AY152132S1	AY152132 Dengue v1
C 30	25	89.3	2552	14	AY152136S1	AY152136 Dengue v1
C 31	25	89.3	2552	14	AY152140S1	AY152140 Dengue v1
C 32	25	89.3	2552	14	AY152144S1	AY152144 Dengue v1
C 33	25	89.3	2552	14	AY152148S1	AY152148 Dengue v1
C 34	25	89.3	2552	14	AY152152S1	AY152152 Dengue v1
C 35	25	89.3	2552	14	AY152156S1	AY152156 Dengue v1
C 36	25	89.3	2552	14	AY152160S1	AY152160 Dengue v1
C 37	25	89.3	2552	14	AY152164S1	AY152164 Dengue v1
C 38	25	89.3	2552	14	AY152168S1	AY152168 Dengue v1
C 39	25	89.3	2552	14	AY152172S1	AY152172 Dengue v1
C 40	25	89.3	2552	14	AY152176S1	AY152176 Dengue v1
C 41	25	89.3	2552	14	AY152180S1	AY152180 Dengue v1
C 42	25	89.3	2552	14	AY152184S1	AY152184 Dengue v1
C 43	25	89.3	2552	14	AY152188S1	AY152188 Dengue v1
C 44	25	89.3	2552	14	AY152192S1	AY152192 Dengue v1
C 45	25	89.3	2552	14	AY152196S1	AY152196 Dengue v1
C 46	25	89.3	2552	14	AY152200S1	AY152200 Dengue v1

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
S66064 structural polypeptide (dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt).
S66064
S66064.1 GI:432575
Dengue virus type 4
Dengue virus type 4
Viruses; serRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2319)
Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
Genetic determinants of dengue type 4 virus neurovirulence for mice

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J. Virol. 67 (11), 6567-6575 (1993)
94016840
8411360
GenBank staff at the National Library of Medicine created this
entry [NCBI gisseq 138430] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
FEATURES
    source
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            /organism="Dengue virus type 4"
            /mol_type="genomic DNA"
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    CDS
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ORIGIN
    Query Match      89.3%; Score 25; DB 14; Length 2319;
    Best Local Similarity 89.3%; Pred. No. 0.89;
    Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
    ||||| ||| ||||| ||||| |||||
DB 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 2
AF469175/c
LOCUS
DEFINITION
Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION
AF469175
VERSION
AF469175.1 GI:18766554
KEYWORDS
Dengue virus type 2
SOURCE
Unpublished
ORGANISM
Nanhai, Guangdong, China
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Direct Submission
JOURNAL
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
FEATURES
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            /protein_id="AAL79018.1"
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            /translation="MNRQKKATVPFNNMLKRRNRVSTVQQLTKRPSLGMQLQGRGPL"

J. Virol. 67 (11), 6567-6575 (1993)
94016840
8411360
GenBank staff at the National Library of Medicine created this
entry [NCBI gisseq 138430] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
FEATURES
    source
        1..2319
            /organism="Dengue virus type 4"
            /mol_type="genomic DNA"
            /db_xref="taxon:11070"
    gene
        1..2319
            /gene="structural polyprotein"
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ORIGIN
    Query Match      89.3%; Score 25; DB 14; Length 2319;
    Best Local Similarity 89.3%; Pred. No. 0.89;
    Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
    ||||| ||| ||||| ||||| |||||
DB 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 3
AF469176/c
LOCUS
DEFINITION
Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION
AF469176
VERSION
AF469176.1 GI:18766556
KEYWORDS
Dengue virus type 2
SOURCE
Unpublished
ORGANISM
Nanhai, Guangdong, China
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Direct Submission
JOURNAL
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
FEATURES
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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2325;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTCTCANNATCCCTGCTGTGG 181

RESULT 4

AR232496/c AR232496 2357 bp RNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 1 from patent US 6455509.
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2357)
AUTHORS Kocheil,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies
JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 228 CCCATCTCTCAGTATCCCTGCTGTGG 201

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DEN2NGC/c DEN2NGC 2357 bp RNA linear VRL 29-MAY-2002
LOCUS
DEFINITION Dengue virus type 2 gene for polyprotein, partial cds, strain:New
Guinea C.
ACCESSION D00346
VERSION D00346.1 GI:221230
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2357)

REFERENCE
AUTHORS Gruenberg,A., Woo,W.S., Biedrzycka,A. and Wright,P.J.
TITLE Partial nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue virus type 2, New Guinea C and
PUO-218 strains
JOURNAL J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
MEDLINE 88258474

3385407
PUBMED
COMMENT Nucleotide 1 in the NGC sequence corresponds to nucleotide 77
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FEATURES

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861..2345
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2346..>2357
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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 228 CCCATCTCTCAGTATCCCTGCTGTGG 201

RESULT 6

AY152036S1/c AY152036S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
SEGMENT 1 of 4
SOURCE
ORGANISM
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
REFERENCE
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vornham,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,


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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTNTCANNATCCCTGCTGTTGG 28
    ||||| ||| ||||| ||||| |||||
Db 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 9
AY152048S1/c
LOCUS          AY152048S1      2552 bp      RNA      linear      VRL 29-SEP-2003
DEFINITION     Dengue virus type 4 D4.14_1998 polyprotein precursor, gene, partial
cds
ACCESSION      AY152048
VERSION        AY152048.1  GI:28170833
KEYWORDS
SEGMENT
SOURCE
ORGANISM       1 of 4
               Dengue virus type 4 (DEN-4)
               Dengue virus type 4
               Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Flavivirus; Dengue virus group.
REFERENCE      1 (bases 1 to 2552)
AUTHORS        Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
               Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
               Selection-Driven Evolution of Emergent Dengue Virus
               Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
               12832629
TITLE          2 (bases 1 to 2552)
JOURNAL        Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
               Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
               Direct Submission
               Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
               Piedras, PO Box 23360, San Juan 00931, Puerto Rico
               Location/Qualifiers
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 10
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DEFINITION     Dengue virus type 4 D4.12_1998 polyprotein precursor, gene, partial
cds
ACCESSION      AY152052
VERSION        AY152052.1  GI:28170842
KEYWORDS
SEGMENT
SOURCE
ORGANISM       1 of 4
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               Dengue virus type 4
               Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Flavivirus; Dengue virus group.
REFERENCE      1 (bases 1 to 2552)
AUTHORS        Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
               Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
               Selection-Driven Evolution of Emergent Dengue Virus
               Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
               12832629
TITLE          2 (bases 1 to 2552)
JOURNAL        Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
               Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
               Direct Submission
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               Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178

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LOCUS AY152056S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.17_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152056
VERSION AY152056.1 GI:28170851
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
ORGANISM Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
Location/Qualifiers
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ORIGIN

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Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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Best Local Similarity 89.3%; Pred. No. 0.88;
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178

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LOCUS AY152060S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.45_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152060
VERSION AY152060.1 GI:28170860
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
ORGANISM Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178

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DEFINITION Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial cds.
ACCESSION AV152064
VERSION AV152064.1 GI:28170869
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
AUTHORS
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
DIRECT SUBMISSION
TITLE
JOURNAL
PUBMED
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
DIRECT SUBMISSION
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178

RESULT 14
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LOCUS
DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial cds.
ACCESSION AV152072
VERSION AV152072.1 GI:28170887
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
AUTHORS
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
DIRECT SUBMISSION
TITLE
JOURNAL
PUBMED
12832629
REFERENCE
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
DIRECT SUBMISSION
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JOURNAL
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LVLTGTSNRNTSMATCIAVGGITLFLGFTVQADMGCVSVWSGRELKCSGIFVVDN
VHTWTEQYKFQEPESPARLASAILNAHKDGVCGIRSTTRLENVWMKQITNELN"

ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
||||| ||| ||||| |||||
Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629

REFERENCE
AUTHORS

2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

TITLE
JOURNAL

Location/Qualifiers
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FEATURES
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VTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSGHVTATITPRSPV
EVKLDPYGLTLDCEPRSGIDNEMILMKKKTWLVHKKWFLDLPLPWTAGADTSEV
HNNYKERMTFKVPHAKRODVTVLGSGEGAMHSLAGATEVSDGDGNHMFAGHLCKV
RMEKLRIKGSYTHCSGKFSIDKEMAEIQHTGTVVKVYEGAGAPCKVPIEIRDVNKE
KVYGRVISSTPLAENTNSVTNIELEPPFGDSYIVIGVNSALTLHWRKGSSTIGKMPF
SYVRGAKRMALGETAMDVGSGGLFTSLGKAVHQVFGSVYTTMFGVSWMIRILIGF
LVLWIGTNSRNTSMAMTCIAVGITLFLGFTVQADMGCVVWSGRELKCGSGIFVVDN
VHTWTQYKFPQSPARLASAILNAHKDGVCGIRSTTRLENVNMVKQITNELN"

CDS

ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 205 CCCATCTCTCAGAAATCCCTGCTGTTGG 178

Search completed: August 3, 2004, 19:08:56
Job time : 686.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 15:36:33 ; Search time 152.5 Seconds
(without alignments)
779.997 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28
Sequence: 1 cccatctcctcannatccctgtgtgg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	89.3	28	7 ABX15697	Abx15697 Dengue vi
C 2	25	89.3	2357	7 ABX13740	Abx13740 Dengue vi
C 3	25	89.3	10616	7 AAD53912	Aad53912 Dengue vi
C 4	25	89.3	10649	7 AAD53911	Aad53911 Recombina
C 5	25	89.3	10649	7 AAD53910	Aad53910 Dengue vi
C 6	25	89.3	10717	4 AAD14605	Aad14605 Dengue vi
C 7	25	89.3	10723	2 AAT49303	Aat49303 cDNA sequ
C 8	25	89.3	10723	2 AAT49304	Aat49304 cDNA enco
C 9	25	89.3	10723	4 AAD14614	Aad14614 Dengue vi
C 10	25	89.3	10723	4 AAD14607	Aad14607 Wild-type
C 11	25	89.3	10723	4 AAD14606	Aad14606 Dengue vi
C 12	25	89.3	10723	4 AAD14608	Aad14608 Attenuate
C 13	25	89.3	10756	4 AAD14609	Aad14609 Dengue vi
C 14	23.4	83.6	32	2 AAT75919	Aat75919 DEN-2 clo
C 15	23.4	83.6	10648	4 AAD14612	Aad14612 Wild-type
C 16	23.4	83.6	10648	4 AAD14613	Aad14613 Attenuate
C 17	23.4	83.6	10723	2 AAT42787	Aat42787 Dengue 2
C 18	21.8	77.9	3381	2 AAT47666	Aat47666 Dengue vi
C 19	20.8	72.1	3381	2 AAX25114	Aax25114 Dengue vi
C 20	20.2	72.1	2394	2 AAT49305	Aat49305 Nucleotid
C 21	20.2	72.1	10718	2 AAO51476	Aag51476 DEN1-S275
C 22	20.2	72.1	10723	4 AAD14603	Aad14603 Dengue vi
C 23	20.2	72.1	10723	4 AAD14604	Aad14604 Dengue vi

ALIGNMENTS

RESULT 1

ABX15697

ID ABX15697 standard; DNA; 28 BP.

XX

AC ABX15697;

XX

DT 31-MAR-2003 (first entry)

XX

DE Dengue virus detection PCR primer #1.

XX

KW PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;

KW dengue haemorrhagic fever; virus; viral detection.

XX

OS Dengue virus.

XX

FH Key Location/Qualifiers

FT modified_base 9

FT /tag= a

FT /mod_base= i

FT /note= "deoxy-inosine"

FT modified_base 13

FT /tag= b

FT /mod_base= i

FT /note= "deoxy-inosine"

FT modified_base 14

FT /tag= c

FT /mod_base= i

FT /note= "deoxy-inosine"

US2002155435-A1.

24-OCT-2002.

28-FEB-2002; 2002US-00085944.

01-MAR-2001; 2001US-0272535P.

(WANG/) WANG W.

Wang W;

WPI; 2003-182625/18.

PT New dengue virus-specific primers, useful for reverse transcriptase-
polymerase chain reaction assays, particularly for detecting or
quantitating dengue virus in a sample.


```
FT mat_peptide /product= "2K protein"  
FT 6826..7560  
FT /*tag= m  
FT  
FT mat_peptide /product= "NS4B protein"  
FT 7561..10260  
FT /*tag= n  
FT /product= "NS5 protein"  
XX  
PN WO200295075-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 22-MAY-2002; 2002WO-US016308.  
XX  
XX 22-MAY-2001; 2001US-0293049P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX (BLAN/) BLANEY J E.  
XX  
XX Whitehead SS, Murphy BR, Hanley KA;  
XX  
XX WPI; 2003-120809/11.  
XX P-PSDB; AAE35314.  
XX  
XX New mutated flavivirus, useful for fine tuning the attenuation and growth  
XX characteristics of dengue virus vaccines for the prevention and/or  
XX treatment of dengue virus infection.  
XX  
XX Disclosure; Page 135-138; 246pp; English.  
XX  
XX The present invention relates to novel mutated flaviviruses comprising a  
XX phenotype in which the viral genome is modified by introduction of a  
XX mutation, singly or in combination, taken from mutations from recombinant  
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation  
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate  
XX dengue type 4 virus. The methods and compositions of the invention are  
XX useful for fine tuning the attenuation and growth characteristics of  
XX dengue virus vaccines for the prevention and/or treatment of dengue virus  
XX infection. The present sequence is Dengue virus type 4 strain  
XX rDEN2/4delta30 DNA  
XX  
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;  
SQ  
  
Query Match 89.3%; Score 25; DB 7; Length 10616;  
Best Local Similarity 89.3%; Pred. No. 0.37;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 CCCATCTTCANNATCCCTGCTGTTGG 28  
DB 304 CCCATCTTCAGTATCCCTGCTGTTGG 277  
  
RESULT 4  
AAD53911/C  
ID AAD53911 standard; DNA; 10649 BP.  
XX  
XX AAD53911;  
XX  
XX 28-MAY-2003 (first entry)  
XX  
XX Recombinant dengue virus type 4 strain rDEN4 DNA.  
DE  
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.  
KW  
XX Dengue virus.  
OS  
XX Key Location/Qualifiers  
FH 102..10649  
FT /*tag= a  
FT /product= "DEN4 strain rDEN4 protein"  
FT 102..440  
FT mat_peptide /tag= c  
FT /product= "Anchored capsid protein"  
FT
```

```
FT mat_peptide 102..398  
FT /*tag= b  
FT /product= "Virion capsid protein"  
FT 441..938  
FT /*tag= d  
FT /product= "Membrane precursor protein"  
FT 714..938  
FT /*tag= e  
FT /product= "Membrane protein"  
FT 939..2423  
FT /*tag= f  
FT /product= "Envelope protein"  
FT 2424..3479  
FT /*tag= g  
FT /product= "NS1 protein"  
FT 3480..4133  
FT /*tag= h  
FT /product= "NS2A protein"  
FT 4134..4523  
FT /*tag= i  
FT /product= "NS2B protein"  
FT 4524..6377  
FT /*tag= j  
FT /product= "NS3 protein"  
FT 6378..6758  
FT /*tag= k  
FT /product= "NS4A protein"  
FT 6638..7562  
FT /*tag= m  
FT /product= "NS4B protein"  
FT 6759..6827  
FT /*tag= l  
FT /product= "2K protein"  
FT 7563..10262  
FT /*tag= n  
FT /product= "NS5 protein"  
XX  
XX WO200295075-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 22-MAY-2002; 2002WO-US016308.  
XX  
XX 22-MAY-2001; 2001US-0293049P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX (BLAN/) BLANEY J E.  
XX  
XX Whitehead SS, Murphy BR, Hanley KA;  
XX  
XX WPI; 2003-120809/11.  
XX P-PSDB; AAE35313.  
XX  
XX New mutated flavivirus, useful for fine tuning the attenuation and growth  
XX characteristics of dengue virus vaccines for the prevention and/or  
XX treatment of dengue virus infection.  
XX  
XX Disclosure; Page 131-132; 246pp; English.  
XX  
XX The present invention relates to novel mutated flaviviruses comprising a  
XX phenotype in which the viral genome is modified by introduction of a  
XX mutation, singly or in combination, taken from mutations from recombinant  
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation  
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate  
XX dengue type 4 virus. The methods and compositions of the invention are  
XX useful for fine tuning the attenuation and growth characteristics of  
XX dengue virus vaccines for the prevention and/or treatment of dengue virus  
XX infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA  
XX  
XX Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;  
SQ  
  
Query Match 89.3%; Score 25; DB 7; Length 10649;  
Best Local Similarity 89.3%; Pred. No. 0.37;
```

```
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 306 CCCATCTCTTCAGAAATCCCTGCTGTGG 279

RESULT 5
AAD53910/c
ID AAD53910 standard; DNA; 10649 BP.
XX AAD53910;
XX
XX 28-MAY-2003 (first entry)
XX Dengue virus type 4 strain 2A DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX Dengue virus.
XX
XX Key Location/Qualifiers
XX CDS 102..10649
XX /tag= a
XX /product= "DEN4 strain 2A protein"
XX mat_peptide 102..440
XX /tag= c
XX /product= "Anchored capsid protein"
XX mat_peptide 102..398
XX /tag= b
XX /product= "Virion capsid protein"
XX mat_peptide 441..938
XX /tag= d
XX /product= "Membrane precursor protein"
XX mat_peptide 714..938
XX /tag= e
XX /product= "Membrane protein"
XX mat_peptide 939..2423
XX /tag= f
XX /product= "Envelope protein"
XX mat_peptide 2424..3479
XX /tag= g
XX /product= "NS1 protein"
XX mat_peptide 3480..4133
XX /tag= h
XX /product= "NS2A protein"
XX mat_peptide 4134..4523
XX /tag= i
XX /product= "NS2B protein"
XX mat_peptide 4524..6377
XX /tag= j
XX /product= "NS3 protein"
XX mat_peptide 6378..6758
XX /tag= k
XX /product= "NS4A protein"
XX mat_peptide 6759..6827
XX /tag= l
XX /product= "2K protein"
XX mat_peptide 6828..7562
XX /tag= m
XX /product= "NS4B protein"
XX mat_peptide 7563..10262
XX /tag= n
XX /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX

(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(BLAN/) BLANEY J E.
Whitehead SS, Murphy BR, Hanley KA;
WPI; 2003-120809/11.
P-PSDB; AAE35312.
New mutated flavivirus, useful for fine tuning the attenuation and growth
characteristics of dengue virus vaccines for the prevention and/or
treatment of dengue virus infection.
Disclosure; Page 123-126; 246pp; English.
The present invention relates to novel mutated flaviviruses comprising a
phenotype in which the viral genome is modified by introduction of a
mutation, singly or in combination, taken from mutations from recombinant
virus bearing Vero adaptation mutations, putative Vero cell adaptation
mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
dengue type 4 virus. The methods and compositions of the invention are
useful for fine tuning the attenuation and growth characteristics of
dengue virus vaccines for the prevention and/or treatment of dengue virus
infection. The present sequence is Dengue virus type 4 strain 2A DNA
SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 7; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 306 CCCATCTCTTCAGAAATCCCTGCTGTGG 279

RESULT 6
AAD14605/c
ID AAD14605 standard; cDNA; 10717 BP.
XX AAD14605;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX Dengue virus; type II.
XX Dengue virus; type III.
XX Chimeric.
XX Key Location/Qualifiers
XX CDS 97..10266
XX /tag= a
XX /product= "DEN-2/3-VP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07984.
XX
```

PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 2; Page 203-219; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/3-VLP fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10717;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 304 CCCATCTCTCAATATCCCTGCTGTGG 277

RESULT 7
AAT49303/C
ID AAT49303 standard; cDNA; 10723 BP.
XX
AC AAT49303;
XX
XX 27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
XX
DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
OS
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 polyprotein
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
XX
XX WO9640933-A1.
PN
XX
XX 19-DEC-1996.
PD
XX
XX 06-JUN-1996; 96WO-US009209.
PF
XX
XX 07-JUN-1995; 95US-00483292.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
PA
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;

XX
DR WPI; 1997-052330/05.
XX P-PSDB; AAW06590.
XX
PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 23; Page 107-121; 261pp; English.
XX
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, PDK
CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
CC -53, may be used in the production of a quadravalent vaccine which
CC provides immunity against all four serotypes of dengue virus. The vaccine
CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
CC protect against infection by all four serotypes of dengue virus, DEN-1,
CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
CC to produce the recombinant protein products of the DNA constructs which
CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;

Query Match 89.3%; Score 25; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 304 CCCATCTCTCAATATCCCTGCTGTGG 277

RESULT 8
AAT49304/C
ID AAT49304 standard; cDNA; 10723 BP.
XX
AC AAT49304;
XX
XX 27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
XX
DE cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
OS
XX
FH Key Location/Qualifiers
FT mutation 57
FT /*tag= b
FT /note= "C>T mutation"
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 attenuated polyprotein
FT /transl_except(pos:643..645, aa:Xaa)
FT /transl_except(pos:1135..1137, aa:Xaa)
FT /transl_except(pos:1393..1395, aa:Xaa)
FT /transl_except(pos:2809..2811, aa:Xaa)
FT /transl_except(pos:3040..3042, aa:Xaa)
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
FT mutation 524
FT /*tag= c
FT /note= "A>T mutation, causes Asp to Val substitution"
FT mutation 2055
FT /*tag= d

```

FT mutation /note= "C>T mutation"
FT 2579 /*tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018 /*tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547 /*tag= g
FT /note= "C>T mutation"
FT 6599 /*tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571 /*tag= i
FT /note= "C>T mutation"
XX
PN WO9640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapratavi N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX WPI; 1997-0523330/05.
XX P-PSDB; AAW06591.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polypeptide from an attenuated derivative of
XX Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
XX polypeptide comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
XX NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
XX production of a quadravalent vaccine which provides immunity against all
XX four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
XX -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
XX The new quadravalent vaccines are used to protect against infection by
XX all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
XX can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
XX syndrome (DHF/DSS). Host cells are used to produce the recombinant
XX protein products of the DNA constructs which are used in the vaccines.
XX (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;
Query Match 89.3%; Score 25; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCMTCAANNATCCCTGCTGTGG 28
| | | | | | | | | | | | | | | | | |
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 9
AAD14614/c
ID AAD14614 standard; cDNA; 10723 BP.
XX
XX AAD14614;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

```

```

XX Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
DE
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
OS
XX Dengue virus; type II.
OS
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 97..10272
XX /*tag= a
XX /product= "DEN-2/1-VP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratavi N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07993.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 5; Page 422-438; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX premembrane/membrane protein (prM) and an envelope protein (E) from wild-
XX type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCMTCAANNATCCCTGCTGTGG 28
| | | | | | | | | | | | | | | | | |
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 10
AAD14607/c
ID AAD14607 standard; cDNA; 10723 BP.
XX
XX AAD14607;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

```

```
DE Wild-type, virulent DEN-2 16681 cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
OS Dengue virus; type II.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 16681 protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07986.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 252-268; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, pramembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCATCTGTCATCAATCCCTGCTGTGG 28
DB 304 CCCATCTGTCATCAATCCCTGCTGTGG 277
RESULT 11
AADI4606/c
ID AADI4606 standard; cDNA; 10723 BP.
XX
AC AADI4606;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
XX
```

```
DE Dengue virus (DEN)-2/4-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS Dengue virus; type IV.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/4-VP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07985.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 227-243; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, pramembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCATCTGTCATCAATCCCTGCTGTGG 28
DB 304 CCCATCTGTCATCAATCCCTGCTGTGG 277
RESULT 12
AADI4608/c
ID AADI4608 standard; cDNA; 10723 BP.
XX
AC AADI4608;
XX
DT 01-NOV-2001 (first entry)
DT Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
XX
```

KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW sa.

XX Dengue virus; type II.

OS Synthetic.

XX Key Location/Qualifiers

FT mutation replace(57, C)

FT mutation /*tag= b

FT CDS 97..10272

FT /*tag= a

FT /*product= "DEN-2 PDK-53 protein variant"

FT mutation replace(524, A)

FT /*tag= C

FT mutation replace(2055, C)

FT /*tag= d

FT mutation replace(2579, G)

FT /*tag= e

FT mutation replace(4018, C)

FT /*tag= f

FT mutation replace(5270, A)

FT /*tag= g

FT mutation replace(5547, T)

FT /*tag= h

FT mutation replace(6599, G)

FT /*tag= i

FT mutation replace(8571, C)

FT /*tag= j

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07987.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for

XX vaccinating against a range of dengue viruses.

XX Example 1; Page 276-292; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras

XX comprising amino acid mutations in the non-structural proteins of a

XX flavivirus. Chimeric viruses containing the attenuation-mutated non-

XX structural genes of the virus are used as a backbone into which the

XX structural protein genes of a second flavivirus strain are inserted.

XX These chimeric viruses elicit pronounced immunogenicity but lack the

XX accompanying clinical symptoms of viral disease. Attenuated chimeric

XX flaviviruses are combined in a pharmaceutical composition to confer

XX simultaneous immunity against several strains of pathogenic flaviviruses

XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

XX flavivirus chimeras are also used as immunogens or multivalent vaccines

XX to confer simultaneous protection against infections. The present cDNA

XX sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant

XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1

XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome

XX contains 5' non-coding region followed by a capsid protein (C) encoding

XX region, premembrane/membrane protein (prM) encoding region, an envelope

XX protein (E) encoding region, followed by the region encoding non-

XX structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'

XX non-coding region

XX Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28

DB 304 CCCATCTCTCAATATCCCTGCTGTTGG 277

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Query Match	89.3%;	Score 25;	DB 4;	Length 10756;	
Best Local Similarity	89.3%;	Pred. NO. 0.37;			
Matches	25;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1	CCCATCTCTCANNATCCCTGCTGTGG	28		
Db	304	CCCATCTCTCANNATCCCTGCTGTGG	277		
RESULT 14					
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ID	AAT75919	standard; DNA; 32 BP.			
XX	AC	AAT75919;			
XX	DT	15-SEP-1997 (first entry)			
XX	DE	DEN-2 cloning/sequencing sense primer, D2-274.			
XX	DEN-2	cloning/sequencing sense primer, D2-274.			
XX	DEN-2	virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;			
XX	NS4A; NS4B; NS5;	PDK-53; quadravalent vaccine; immunity; serotype;			
XX	chimeric DEN-2/1 virus;	chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;			
XX	dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;				
XX	DHF; DSS; PCR; amplify;	polymerase chain reaction; primer; ss.			
XX	Synthetic.				
XX	OS				
XX	WO9640933-Al.				
XX	PN	19-DEC-1996.			
XX	PD	06-JUN-1996; 96WO-US009209.			
XX	PF	07-JUN-1995; 95US-00483292.			
XX	PR	(USSH) US DEPT HEALTH & HUMAN SERVICES.			
XX	PA	(UYMA-) UNIV MAHIDOL AT SALAYA.			
XX	PI	Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;			
XX	PI	Kinney R, Trent DW;			
XX	PI	WPI; 1997-052330/05.			
XX	DR	PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -			
XX	CC	also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a			
XX	CC	quadravalent vaccine for protecting against Dengue virus infection.			
XX	CC	Example; Page 100; 261pp; English.			
XX	CC	The sequences given in AAT75909-T76029 are primers which were used in the			
XX	CC	amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the			
XX	CC	invention. The Dengue 2 viral DNA encodes a polyprotein which comprises			
XX	CC	the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.			
XX	CC	The quadravalent vaccine of the invention comprises an attenuated Dengue			
XX	CC	virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3			
XX	CC	virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are			
XX	CC	used to protect against infection by all four serotypes of dengue virus,			
XX	CC	DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal			
XX	CC	dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are			
XX	CC	used to produce the recombinant protein products of the DNA constructs			
XX	CC	which are used in the vaccines			
XX	CC				
XX	SQ	Sequence 32 BP; 12 A; 7 C; 10 G; 3 T; 0 U; 0 Other;			
Query Match	83.6%;	Score 23.4;	DB 2;	Length 32;	
Best Local Similarity	85.7%;	Pred. NO. 0.74;			
Matches	24;	Conservative	0;	Mismatches	4;
				Indels	0;
				Gaps	0;
QY	1	CCCATCTCTCANNATCCCTGCTGTGG	28		
Db	31	CCCATCTCTCAGTATCCCTGCTGTGG	4		

Search completed: August 3, 2004, 18:46:01
Job time : 155.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:28:49 ; Search time 37 Seconds
(without alignments)
419.963 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccatctcctcannatccctgtgttg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A-COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B-COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A-COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	89.3	2357	4	US-08-869-423-1
C 2	21.8	77.9	3381	3	US-08-937-195-1
C 3	21.8	77.9	3381	3	US-08-937-195-2
C 4	21.8	77.9	3381	3	US-08-915-152-1
C 5	21.8	77.9	3381	3	US-08-915-152-2
C 6	21.8	77.9	3381	5	PCT-US96-07627-1
C 7	21.8	77.9	3381	5	PCT-US96-07627-2
C 8	20.2	72.1	10718	3	US-08-325-425B-1
C 9	18.8	67.1	5674	1	US-07-807-043B-8
C 10	18.8	67.1	5674	1	US-08-190-411A-1
C 11	18.8	67.1	5674	1	US-08-299-849B-8
C 12	18.8	67.1	5674	2	US-08-560-024-1
C 13	18.8	67.1	5674	2	US-08-142-368A-8
C 14	18.8	67.1	5674	2	US-08-967-727-8
C 15	18.8	67.1	5674	3	US-08-037-230D-8
C 16	18.8	67.1	5674	4	US-09-583-850-8
C 17	18.8	67.1	5674	4	US-09-579-197-8
C 18	18.8	67.1	5674	4	US-09-404-026-8
C 19	18.8	67.1	5674	4	US-09-312-464-8
C 20	18.8	67.1	5707	2	US-08-472-809B-8
C 21	18.8	67.1	6345	2	US-08-472-809B-7
C 22	18.2	65.0	2917	2	US-08-437-607A-3
C 23	18.2	65.0	3030	4	US-09-439-313-333
C 24	18.2	65.0	3030	4	US-09-352-616A-333
C 25	18.2	65.0	3030	4	US-09-232-149A-333
C 26	18.2	65.0	3030	4	US-09-636-215-333
C 27	18.2	65.0	3030	4	US-09-685-166A-333

C 28	18.2	65.0	3030	4	US-09-688-489-333	Sequence 333, App
C 29	18.2	65.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 30	17.6	62.9	1064	2	US-08-529-878B-40	Sequence 40, Appli
C 31	17.6	62.9	1514	4	US-09-023-655-1316	Sequence 1316, Ap
C 32	17.6	62.9	2238	1	US-08-389-668A-1	Sequence 1, Appli
C 33	17.6	62.9	2238	1	US-08-732-506-1	Sequence 1, Appli
C 34	17.6	62.9	2238	5	PCT-US95-05768-1	Sequence 11, Appli
C 35	17.6	62.9	19025	4	US-09-849-334-3	Sequence 3, Appli
C 36	17.6	62.9	19025	4	US-10-274-878-3	Sequence 3, Appli
C 37	17.6	62.9	31960	4	US-09-453-702B-11	Sequence 11, Appli
C 38	17.2	61.4	1310	4	US-09-976-594-926	Sequence 926, App
C 39	17.2	61.4	5410	4	US-09-561-818A-7	Sequence 7, Appli
C 40	17.2	61.4	5498	4	US-09-561-818A-5	Sequence 5, Appli
C 41	17.2	61.4	5942	4	US-09-561-818A-3	Sequence 3, Appli
C 42	17.2	61.4	6204	4	US-09-561-818A-1	Sequence 1, Appli
C 43	17	60.7	1867	4	US-09-976-594-631	Sequence 631, App
C 44	17	60.7	4629	2	US-08-484-891-7	Sequence 7, Appli
C 45	17	60.7	4629	4	US-09-150-811-7	GENERAL INFORMA

ALIGNMENTS

RESULT 1
US-08-869-423-1/c
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kalish, Daniel
; REGISTRATION NUMBER: 33,599
; REFERENCE/DOCKET NUMBER: NC 77,654
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-5642
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

```
/ ORGANISM: Dengue virus
/ STRAIN: New Guinea C
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: Prem and Envelope
/ MAP POSITION: 330-2446
/ UNITS: bp
/ PUBLICATION INFORMATION:
/ AUTHORS: Gruenberg, A
/ AUTHORS: Woo, W S
/ AUTHORS: Biedrzycka, A
/ AUTHORS: Wright, P J
/ TITLE: Partial nucleotide sequence and deduced amino
/ TITLE: acid sequence of the structural proteins of dengue
/ TITLE: virus type 2, New Guinea C and PUO-218 strains
/ JOURNAL: J. Gen. Virol.
/ VOLUME: 69
/ PAGES: 1391-1398
/ DATE: 1988
/ PUBLICATION INFORMATION:
/ AUTHORS: Irie, K
/ AUTHORS: Mohan, P M
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Putnak, R
/ AUTHORS: Padmanabhan, R
/ TITLE: Sequence Analysis of Cloned dengue virus type
/ TITLE: 2 genome (New Guinea-C strain)
/ JOURNAL: Gene
/ VOLUME: 75
/ ISSUE: 2
/ PAGES: 197-211
/ DATE: 1989
/ PUBLICATION INFORMATION:
/ AUTHORS: Yaegashi, T
/ AUTHORS: Vakharia, V N
/ AUTHORS: Page, K
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Feighny, R
/ AUTHORS: Padmanabhan, R
/ JOURNAL: Gene
/ VOLUME: 46
/ ISSUE: 2-3
/ PAGES: 257-267
/ DATE: 1986
/ US-08-869-423-1

Query Match 89.3%; Score 25; DB 4; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.023;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 228 CCCATCTCTCAGTATCCCTGCTGTGG 201

RESULT 2
US-08-937-195-1/c
/ Sequence 1, Application US/08937195
/ Patent No. 6136561
/ GENERAL INFORMATION:
/ APPLICANT: IVY, JOHN M.
/ APPLICANT: KAKANO, EILEEN
/ APPLICANT: CLEMENTS, DAVID
/ TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1812
/ COMPUTER READABLE FORM:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-1
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTTGG 181
RESULT 3
US-08-937-195-2/c
Sequence 2, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVI, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: Strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-2
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
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Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 4
US-08-915-152-1/c
; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-1
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 5
US-08-915-152-2/c
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
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; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION: 435
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEFAX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-2
; Query Match 77.9%; Score 21.8; DB 3; Length 3381;
; Best Local Similarity 82.1%; Pred. No. 0.75;
; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
; QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
; DB 208 CCCATCTTTTAAATATCCCTGCTGTGG 181
; RESULT 6
; PCT-US96-07627-1/c
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
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/ OTHER INFORMATION: Wild-Type sequence"
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/ NAME/KEY: misc_feature
/ LOCATION: 1762_ /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1929_ /note= "C is replaced by T for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2310_ /note= "A is replaced by N for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid."
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 616_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Membrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 841_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Envelope"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2326_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for NS1"
/ PUBLICATION INFORMATION:
/ AUTHORS: Hahn, Y.S.
/ JOURNAL: Virology
/ VOLUME: 162
/ PAGES: 167-180
/ DATE: 1988
PCT-US96-07627-1
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Query Match 77.9%; Score 21.8; DB 5; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
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Db 208 CCCATCTTTTATATATCCCTGCTGTGG 181
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RESULT 7
PCT-US96-07627-2/c
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/07627
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2(DEN-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PR159/S1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3381
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1216_1218
/ OTHER INFORMATION: /note= "GAG(coding for Glu) is
/ OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15:
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1258_1260
/ OTHER INFORMATION: /note= "GTG(coding for Val) is
/ OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15:
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1762_1764
/ OTHER INFORMATION: /note= "ATT(coding for Ile) is
/ OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15:
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1927_1929
/ OTHER INFORMATION: /note= "AGT(Coding for Ser) is
/ OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR15:
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 616_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence of Membrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 841_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence of Envelope"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2326_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for NS1"
/ PUBLICATION INFORMATION:
/ AUTHORS: Hahn, Y.S.
/ JOURNAL: Virology
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RESULT 9

STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: 01-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5541104man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-190-411A-1

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAATCCCTGCTGT 1921

RESULT 11
US-08-299-849B-8
Sequence 8, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-299-849B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAATCCCTGCTGT 1921

RESULT 12
US-08-560-024-1
Sequence 1, Application US/08560024
Patent No. 5843448
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tsang; Stockert, Elisabeth;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,024
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE: 01-FEBRUARY-1994
; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: PCT/US92/04354
; PRIOR APPLICATION DATA:
; FILING DATE: 07/807,043
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; FILING DATE: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; FILING DATE: 07/705,702
; APPLICATION NUMBER: 07/705,702
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5843448man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-08-560-024-1

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 13
US-08-142-368A-8
; Sequence 8, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van den Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: PCT/US92/04354
; PRIOR APPLICATION DATA:
; FILING DATE: 07/807,043
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; FILING DATE: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; FILING DATE: 07/705,702
; APPLICATION NUMBER: 07/705,702
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-08-142-368A-8

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 14
US-08-967-727-8
; Sequence 8, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
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RESULT 15
US-08-037-230D-8
; Sequence 8, Application US/08037230D
; Patent No. 6215525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Fallieur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:40:54 ; Search time 158 Seconds
(without alignments)
868.911 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

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Scoring table: IDENTITY NUC

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Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

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Post-processing: Minimum Match 0%

Maximum Match 100%

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18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	89.3	28	14	US-10-085-944-1
2	21.8	77.9	3381	15	US-10-247-960-2
3	19.2	68.6	691	13	US-10-027-632-281617
4	19.2	68.6	691	16	US-10-027-632-281617
5	18.8	67.1	2739	17	US-10-437-963-62174
6	18.6	66.4	482	15	US-10-029-386-27304
7	18.6	66.4	486	9	US-09-864-761-27448
8	18.6	66.4	577	15	US-10-029-386-13604
9	18.6	66.4	2301	17	US-10-437-963-53513
10	18.6	66.4	6412	17	US-10-322-281-484
11	18.6	66.4	61396	17	US-10-322-281-483
12	18.6	66.4	98634	13	US-10-087-192-1870
13	18.2	65.0	476	10	US-09-814-353-1708
14	18.2	65.0	476	10	US-09-814-353-8061

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15 18.2 65.0 1506 13 US-10-027-632-256653,
16 18.2 65.0 1506 16 US-10-027-632-256653,
17 18.2 65.0 3030 9 US-09-759-143-333
18 18.2 65.0 3030 9 US-09-780-669-333
19 18.2 65.0 3030 9 US-09-822-827-333
20 18.2 65.0 3030 9 US-09-232-880-333
21 18.2 65.0 3030 9 US-09-895-793-333
22 18.2 65.0 3030 9 US-09-895-814-333
23 18.2 65.0 3030 14 US-10-012-896-333
24 18.2 65.0 3030 15 US-10-010-940-333
25 18.2 65.0 3030 15 US-10-144-678A-333
26 18.2 65.0 3030 15 US-10-294-025-333
27 18.2 65.0 77777 17 US-10-318-389-4
28 18.2 65.0 81826 15 US-10-175-523-197
29 17.8 63.6 415 13 US-10-027-632-183225
30 17.8 63.6 415 16 US-10-027-632-183225
31 17.8 63.6 1277 17 US-10-437-963-83170
32 17.8 63.6 90798 17 US-10-318-819A-4
33 17.6 62.9 239 9 US-09-864-761-26181
34 17.6 62.9 353 11 US-09-864-408A-2719
35 17.6 62.9 371 17 US-10-437-963-13942
36 17.6 62.9 410 9 US-09-864-761-21296
37 17.6 62.9 453 10 US-09-918-995-14536
38 17.6 62.9 494 9 US-09-864-761-4549
39 17.6 62.9 566 9 US-09-864-761-9825
40 17.6 62.9 649 13 US-10-027-632-275006
41 17.6 62.9 649 16 US-10-027-632-275006
42 17.6 62.9 700 16 US-10-341-961A-7
43 17.6 62.9 796 13 US-10-027-632-156282
44 17.6 62.9 796 16 US-10-027-632-156282
45 17.6 62.9 858 13 US-10-424-599-106253

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ALIGNMENTS

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RESULT 1
US-10-085-944-1
; Sequence 1, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc feature
; LOCATION: 9 13,14
; OTHER INFORMATION: n = inosine
; US-10-085-944-1

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Query Match 89.3%; Score 25; DB 14; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCATCTCANNATCCCTGCTGTGG 28

Db 1 CCCATCTCANNATCCCTGCTGTGG 28

RESULT 2

US-10-247-960-2/c

; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 09/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match 77.9%; Score 21.8; DB 15; Length 3381;
Best Local Similarity 82.1%; Pred. No. 3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTATATCCCTGCTGTGG 181

RESULT 3
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match 68.6%; Score 19.2; DB 13; Length 691;
Best Local Similarity 77.8%; Pred. No. 42;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 27
Db 562 CCCAGCTCTCTCATGTCCCTGCTGTGG 536

RESULT 4
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

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Best Local Similarity 77.8%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 562 CCCAGCTCTCTCATGTCCCTGCTGTGG 536

RESULT 5
US-10-437-963-62174/c
; Sequence 62174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 62174
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:

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/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharron G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aeomica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666

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Best Local Similarity 75.0%; Pred. No. 1e+02;


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US-09-814-353-1708/c
; Sequence 1708, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1708
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-1708

Query Match 65.0%; Score 18.2; DB 10; Length 476;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 424 CCTTCTCCTCACAGTCCCTGCTG 399

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; Sequence 8061, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8061
; LENGTH: 476
; TYPE: DNA
US-09-814-353-8061/c

Query Match 65.0%; Score 18.2; DB 10; Length 476;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCNTCANNATCCCTGCTGTG 27
DB 424 CCTTCTCCTCACAGTCCCTGCTG 399
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; ORGANISM: Homo sapiens
; Sequence 8061, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256653
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256653

Query Match 65.0%; Score 18.2; DB 13; Length 1506;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 293 CATCTCCTCACAGTCTTGCTGTG 318

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-085-944-1

Perfect score: 28

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	19.2	68.6	287 10	BB338318
2	19.2	68.6	453 28	AQ517624 HS 5140 B
3	19.2	68.6	481 13	EX109154 BX109154
4	19.2	68.6	577 29	CC690447 CGXAB64TH

5	19.2	68.6	646	14	CD443887
6	19.2	68.6	659	29	AG063981 Pan trogl
7	19.2	68.6	938	29	CG232800 OG2BI20TV
8	19.2	68.6	952	29	CG456461 PUIJW63TD
9	19.2	68.6	961	29	CNS06EAJ
10	19.2	68.6	1018	29	CG456420
11	19.2	68.6	1139	28	CC187707
12	19.2	68.6	2314	11	BC026893 Mus muscu
13	18.8	67.1	413	10	BF723268
14	18.8	67.1	445	14	CF546284 lae70C10.
15	18.8	67.1	463	12	BI048424 MR4-TN011
16	18.8	67.1	990	29	CNS01L0W
17	18.8	67.1	2185	29	CG755418
18	18.6	66.4	231	10	BF655438
19	18.6	66.4	231	10	BF655439
20	18.6	66.4	239	9	AV361516
21	18.6	66.4	245	13	BX639040
22	18.6	66.4	274	10	BF40266
23	18.6	66.4	280	10	AW354424
24	18.6	66.4	285	9	AV116369
25	18.6	66.4	297	10	BF600952
26	18.6	66.4	300	10	BF174849
27	18.6	66.4	389	10	BF601010
28	18.6	66.4	411	12	BM286538
29	18.6	66.4	413	9	AA068952 mm61B09.Y
30	18.6	66.4	414	9	AU232945
31	18.6	66.4	420	9	AU232945
32	18.6	66.4	421	10	AW477778
33	18.6	66.4	446	14	CD804048
34	18.6	66.4	472	14	CB418067
35	18.6	66.4	505	12	BM090019
36	18.6	66.4	540	9	AV665694
37	18.6	66.4	550	14	CF162479
38	18.6	66.4	568	28	AQ793162
39	18.6	66.4	598	9	AI390262
40	18.6	66.4	602	13	BO790197
41	18.6	66.4	622	14	CF747473
42	18.6	66.4	625	14	CA371379
43	18.6	66.4	627	28	AZ928229
44	18.6	66.4	677	10	BB478112
45	18.6	66.4	700	12	BI735720

ALIGNMENTS

RESULT 1	BB338318/c	287 bp	linear	EST 11-JUL-2000
LOCUS	BB338318	RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone B930012N10 3', similar to U1352 Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, mRNA		
DEFINITION	BB338318	sequence.		
ACCESSION	BB338318			
VERSION	BB338318.1	GI:9047081		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 287)			
	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Taya, T., Teunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, W. and			


```

TITLE
JOURNAL
COMMENT
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGp998044588
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACGGAACAGCTATGAC.

FEATURES
source
Location/Qualifiers
1..481
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998J044588 ; IMAGE:1873635"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co8"
/note="Organ: Colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 68.6%; Score 19.2; DB 13; Length 481;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 27
|||||
Db 401 CCCACCTCCACAGCATCCCGCTGTGG 427

RESULT 4
CC690447 577 bp DNA linear GSS 19-JUN-2003
LOCUS
DEFINITION
OGXAB64TH ZM.0.7.1.5_KB Zea mays genomic clone ZMMBMA0482K08,
genomic survey sequence.
ACCESSION
CC690447
VERSION
CC690447.1 GI:32095223
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 577)
Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGXAB64TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR

TITLE
JOURNAL
COMMENT
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGp998044588
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACGGAACAGCTATGAC.

FEATURES
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Location/Qualifiers
1..577
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/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0482K08"
/clone_lib="ZM.0.7.1.5_KB"
/note="Vector: pBGSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 577;
Best Local Similarity 77.8%; Pred. No. 3.1e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 146 CCTGCTCGTCAGCATCCCTGCAGTTGG 172

RESULT 5
CD443887 646 bp mRNA linear EST 03-JUN-2003
LOCUS
DEFINITION
ELOIN0432D03.b Endosperm_4 Zea mays cDNA, mRNA sequence.
ACCESSION
CD443887
VERSION
CD443887.1 GI:31359530
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 646)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..646
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 68.6%; Score 19.2; DB 14; Length 646;
Best Local Similarity 77.8%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTGG 27
|||||
Db 276 CCGATGTCATCATTCCTCCGCTGTGG 302

RESULT 6
AG063981/c 659 bp DNA linear GSS 03-NOV-2001
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-052019.F, genomic survey sequence.
ACCESSION
AG063981

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VERSION AG063981.1 GI:16615783
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Totoki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL BAC end sequences of Library PTB
REFERENCE 2 (bases 1 to 659)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Totoki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL Direct Submission
Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source Location/Qualifiers
1 .659
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/db_xref="taxon:9598"
/clone="PTB-052019.F"
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 659;
Best Local Similarity 77.8%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCNCANNATCCCTGCTGTTG 27
Db 626 CCCACCTCCACGATCCCGCTGTTG 600
RESULT 7
CG232800 938 bp DNA linear GSS 22-AUG-2003
LOCUS CG232800
DEFINITION CG2B120TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBma0752D15,
genomic survey sequence.
ACCESSION CG232800
VERSION CG232800.1 GI:34132686
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE Citek, R.W., Nurnberg, A., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
JOURNAL Consortium for Maize Genomics
COMMENT Other GSSs: CG2B120TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843

```

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FEATURES
source Location/Qualifiers
1 .938
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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methylation filtered genomic DNA library"
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Best Local Similarity 77.8%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTGG 28
Db 51 CCTGCTCGTCAGCATCCCTGCACTTGG 77
RESULT 8
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LOCUS PUIJW63TDB_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMMBta0600K05,
genomic survey sequence.
ACCESSION CG456461
VERSION CG456461.1 GI:34841461
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 952)
Whiteaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Bennetzen, J., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUIJW63TBB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source Location/Qualifiers
1 .952
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBta0600K05"
/clone_lib="ZM 0.6 1.0 KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 952;
Best Local Similarity 77.8%; Pred. No. 3.8e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTGG 28
Db 895 CCTGCTCGTCAGCATCCCTGCACTTGG 869

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RESULT 9	CNS06EAJ/c	961 bp	DNA	linear	GSS 17-JUN-2001
LOCUS	T3 end of clone AROAA020A08 of library AROAA from strain CBS 732 of				
DEFINITION	Zygosaccharomyces rouxii, genomic survey sequence.				
ACCESSION	AL394865				
VERSION	AL394865.1	GI:12145083			
KEYWORDS	GSS.				
SOURCE	Zygosaccharomyces rouxii				
ORGANISM	Zygosaccharomyces rouxii				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.				
AUTHORS	1 (bases 1 to 961) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrans,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
JOURNAL	FEMS Lett. 487 (1), 3-12 (2000)				
MEDLINE	20584711				
PUBMED	11152876				
REFERENCE	2 (bases 1 to 961) de Montigny,J., Straub,M., Potier,S., Tekai,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.				
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 8.				
TITLE	Zygosaccharomyces rouxii				
JOURNAL	FEMS Lett. 487 (1), 52-55 (2000)				
MEDLINE	20584718				
PUBMED	11152883				
REFERENCE	3 (bases 1 to 961) Direct Submission				
AUTHORS	Genoscope.				
TITLE	Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage.				
JOURNAL	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)				
MEDLINE	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.				
FEATURES	Location/Qualifiers				
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misc_feature					
ORIGIN					
Query Match	68.6%;	Score 19.2;	DB 29;	Length 961;	
Best Local Similarity	77.8%;	Pred. No. 3.8e+03;			
Matches	21;	Conservative	0;	Mismatches	6;
Indels	0;	Gaps	0;		
QY	1	CCCATCTGTCANNATCCCTGCTGTTG	27		
Db	431	CCTAGTCATTAGTATCCCTGCTGTTG	405		

RESULT 9	CNS06EAJ/c
LOCUS	ZYGOSACCHAROMYCES ROUXII
DEFINITION	T3 end of clone AROAA020A08 of library AROAA from strain CBS 732 of Zygosaaccharomyces rouxii, genomic survey sequence.
ACCESSION	AL394865.1 GI:12145083
VERSION	GSS.
KEYWORDS	SOURCE ORGANISM
ORGANISM	Zygosaaccharomycetes rouxii Zygosaaccharomycetes rouxii Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaaccharomycetes. 1 (bases 1 to 961) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bollotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,A., Dujon,B., Durren,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaiia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEMS Lett. 487 (1), 3-12 (2000)
JOURNAL MEDLINE PUBLISHED	20584711
REFERENCE AUTHORS	11152876 2 (bases 1 to 961) de Montigny,J., Straub,M., Potier,S., Tekaiia,F., DuJon,B., Wincker,P., Artiguenave,F. and Souciet,J. Genomic exploration of the hemiascomycetous yeasts: 8. Zygosaaccharomycetes rouxii FEMS Lett. 487 (1), 52-55 (2000)
JOURNAL MEDLINE PUBLISHED	20584718
REFERENCE AUTHORS	11152883 3 (bases 1 to 961) Direct Submission Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaaccharomycetes rouxii, Saccharomycetes kluyverari, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES source	Location/Qualifiers 1..961 /organism="Zygosaaccharomycetes rouxii" /mol_type="genomic DNA" /strain="CBS 732" /db_xref="taxon:4956" /clone="AROAA020A08" /clone_lib="AR0AA" /note="end : f3"
misc_feature	<3..>419 /note="similar to Saccharomyces cerevisiae ORF YNL289w [pCti ; cyclin, Gl/S-specific]" /evidence=not_experimental
ORIGIN	Query Match 68.6%; Score 19.2; DB 29; Length 961; Best Local Similarity 77.8%; Pred. No. 3.8e+03; Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy	1 CCCATCTGTCANNATCCCTGCTGGTGTG 27
Dd	431 CCTAGTCAATTAGTAGTATCCCTGCTGGTGTG 405

Class: BAC ends
High quality sequence start: 145
High quality sequence stop: 618.

FEATURES

Location/Qualifiers
1..1139
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-33N7"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/notes="Vector: pPARAC2.1; Site 1: EcoRI; CH261 Female Chicken library - For library and clone ordering information: <http://www.chori.org/bacpac>"

ORIGIN

Query Match 68.6%; Score 19.2; DB 28; Length 1139;
Best Local Similarity 77.8%; Pred. No. 4e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28

Db 131 CCAGCTCATCTATATCCTGCTGTGG 157

RESULT 12

BC026893/c
LOCUS
DEFINITION Mus musculus downstream of Skil, mRNA (cDNA clone IMAGE:3982045),
with apparent retained intron.

ACCESSION BC026893.1 GI:22268016

VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 2314)
Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heideh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

PUBMED 12477932

2 (bases 1 to 2314)

Srausberg, R.

Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 40 Row: i Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis

This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers
1..2314

/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3982045"
/tissue_type="Mammary tumor metastasized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
/clone_lib="NCI CGAP_Lu29"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"

ORIGIN

Query Match 68.6%; Score 19.2; DB 11; Length 2314;
Best Local Similarity 77.8%; Pred. No. 5.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 27

Db 1769 CCATCTGTCATCTCCTGCTGTGG 1743

RESULT 13

BF723268/c
LOCUS
DEFINITION mab30a01.y1 Soares NMEBA branchial arch Mus musculus cDNA clone
IMAGE:3971616 5' similar to TR:Q93V6 Q93V6 HYPOTHETICAL 22.9 KD
PROTEIN ;, mRNA sequence.

ACCESSION BF723268.1 GI:12024270

VERSION BF723268

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 413)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESTs: mab30a01.x1

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1471648

laser-captured isthmal cells from tox176 transgenic mice. 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI."

ORIGIN

Best Match 67.1%; Score 18.8; DB 14; Length 445;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTTCNTCANNATCCCTGCTGT 25
||||| ||| ||||| |||||
Db 224 CCAGATCATCAGGATCCCTGCTGT 200

RESULT 15
BI048424/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI048424 463 bp mRNA linear EST 14-JUN-2001
MR4-TN0112-080101-209-e05 TN0112 Homo sapiens cDNA, mRNA sequence.
BI048424
BI048424.1 GI:14455046
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Dias Neto,E., Garcia Correa,R., Varjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-TN0112-
080101-209-e05&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 463.
Location/Qualifiers
1. 463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0112"
/note="Organ: testis normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source

Query Match 67.1%; Score 18.8; DB 12; Length 463;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCATCTCNCANNATCCCTGCTGTT 26
| | | | | | | | | | | | | | | | | | | | | |
Db 43 CCATCCCATCACCAGCCCTGCTGTT 19

Search completed: August 3, 2004, 19:50:54
Job time : 1259 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 17:17:11 ; Search time 685.5 Seconds
(without alignments)
1770.394 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aatatgctgaaacgcgagagaacccgcg 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl:*
- 1: gb_ba:*
 - 2: gb_htg:*
 - 3: gb_in:*
 - 4: gb_om:*
 - 5: gb_ov:*
 - 6: gb_pat:*
 - 7: gb_ph:*
 - 8: gb_pl:*
 - 9: gb_pr:*
 - 10: gb_ro:*
 - 11: gb_sts:*
 - 12: gb_sy:*
 - 13: gb_un:*
 - 14: gb_vi:*
 - 15: em_ba:*
 - 16: em_fun:*
 - 17: em_hum:*
 - 18: em_in:*
 - 19: em_mu:*
 - 20: em_om:*
 - 21: em_or:*
 - 22: em_ov:*
 - 23: em_pat:*
 - 24: em_ph:*
 - 25: em_pl:*
 - 26: em_ro:*
 - 27: em_sts:*
 - 28: em_un:*
 - 29: em_vi:*
 - 30: em_htg_hum:*
 - 31: em_htg_inv:*
 - 32: em_htg_other:*
 - 33: em_htg_mus:*
 - 34: em_htg_pln:*
 - 35: em_htg_rod:*
 - 36: em_htg_mam:*
 - 37: em_htg_vrt:*
 - 38: em_sy:*
 - 39: em_htgo_hum:*
 - 40: em_htgo_mus:*
 - 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28	100.0	342	14	FLD2CPM2	X51709 Dengue-2 vi
2	28	100.0	840	14	AF360860	AF360860 Dengue vi
3	28	100.0	840	14	AF360861	AF360861 Dengue vi
4	28	100.0	840	14	AF360862	AF360862 Dengue vi
5	28	100.0	840	14	AF360863	AF360863 Dengue vi
6	28	100.0	2319	14	S66064	S66064 structural
7	28	100.0	2325	14	AF469175	AF469175 Dengue vi
8	28	100.0	2325	14	AF469176	AF469176 Dengue vi
9	28	100.0	2325	14	AF509530	AF509530 Dengue vi
10	28	100.0	2325	14	AY044442	AY044442 Dengue vi
11	28	100.0	2357	6	AR232496	AR232496 Sequence
12	28	100.0	2357	14	DEN2NGC	D00346 Dengue viru
13	28	100.0	2469	14	DENJAMA	M15075 Dengue viru
14	28	100.0	2552	14	AY152036S1	AY152036 Dengue vi
15	28	100.0	2552	14	AY152040S1	AY152040 Dengue vi
16	28	100.0	2552	14	AY152044S1	AY152044 Dengue vi
17	28	100.0	2552	14	AY152048S1	AY152048 Dengue vi
18	28	100.0	2552	14	AY152052S1	AY152052 Dengue vi
19	28	100.0	2552	14	AY152056S1	AY152056 Dengue vi
20	28	100.0	2552	14	AY152060S1	AY152060 Dengue vi
21	28	100.0	2552	14	AY152064S1	AY152064 Dengue vi
22	28	100.0	2552	14	AY152068S1	AY152068 Dengue vi
23	28	100.0	2552	14	AY152072S1	AY152072 Dengue vi
24	28	100.0	2552	14	AY152076S1	AY152076 Dengue vi
25	28	100.0	2552	14	AY152080S1	AY152080 Dengue vi
26	28	100.0	2552	14	AY152084S1	AY152084 Dengue vi
27	28	100.0	2552	14	AY152088S1	AY152088 Dengue vi
28	28	100.0	2552	14	AY152092S1	AY152092 Dengue vi
29	28	100.0	2552	14	AY152096S1	AY152096 Dengue vi
30	28	100.0	2552	14	AY152100S1	AY152100 Dengue vi
31	28	100.0	2552	14	AY152104S1	AY152104 Dengue vi
32	28	100.0	2552	14	AY152108S1	AY152108 Dengue vi
33	28	100.0	2552	14	AY152112S1	AY152112 Dengue vi
34	28	100.0	2552	14	AY152116S1	AY152116 Dengue vi
35	28	100.0	2552	14	AY152120S1	AY152120 Dengue vi
36	28	100.0	2552	14	AY152124S1	AY152124 Dengue vi
37	28	100.0	2552	14	AY152128S1	AY152128 Dengue vi
38	28	100.0	2552	14	AY152132S1	AY152132 Dengue vi
39	28	100.0	2552	14	AY152136S1	AY152136 Dengue vi
40	28	100.0	2552	14	AY152140S1	AY152140 Dengue vi
41	28	100.0	2552	14	AY152144S1	AY152144 Dengue vi
42	28	100.0	2552	14	AY152148S1	AY152148 Dengue vi
43	28	100.0	2552	14	AY152152S1	AY152152 Dengue vi
44	28	100.0	2552	14	AY152156S1	AY152156 Dengue vi
45	28	100.0	2552	14	AY152160S1	AY152160 Dengue vi

ALIGNMENTS

RESULT 1
FLD2CPM2
LOCUS
DEFINITION
Dengue-2 virus RNA for capsid protein, partial, from a case of
dengue shock syndrome (M2) .
ACCESSION
X51709
VERSION
X51709.1 GI:59299
KEYWORDS
Dengue virus type 2
SOURCE
Dengue virus type 2
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 342)
AUTHORS
Samuel,S., Koh,C.L., Pang,T. and Lam,S.K.
TITLE
Nucleotide and encoded amino acid sequences of the capsid protein

gene of three dengue-2 viruses isolated in Malaysia from patients with dengue haemorrhagic fever, dengue shock syndrome or dengue fever

Nucleic Acids Res. 18 (7), 1904 (1990)

90245598

PUBLISHED

2 (bases 1 to 342)

REFERENCE

Koh, C. L.

Direct Submission

Submitted (05-FEB-1990) Koh C.-L., University of Malaysia,

Department of Genetics and Cellular Biology, 5910 Kuala Lumpur,

Malaysia

See <M15075> and <M19197> for previously reported sequence. See

<X51708> and <X51710> for capsid protein sequences of M1 and M3.

FEATURES

Location/Qualifiers

1..342

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/strain="M2, isolated from case of dengue shock syndrome"

/db_xref="taxon:11060"

1..342

/note="unnamed protein product; capsid protein, partial

(AA 1-114)"

/codon_start=1

/protein_id="CA36005.1"

/db_xref="GI:59300"

/db_xref="GOA:O89715"

/db_xref="SPRMBL:O89715"

/translation="MNDQRKARSTPFNMLKRNVRVSTVQQLTKRFSGLMLOGRGLP

KLFMALVAFRLFTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMNLINRRRTA

GVIIMLIPTVMA"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 342;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

AF360860

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

21571640

PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Direct Submission

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 840;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

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KEYWORDS

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Direct Submission

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 840;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

AF360860

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

Dengue virus type 2

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Flavivirus; Dengue virus group.

1 (bases 1 to 840)

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Holmes, E.C. and Gould, E.A.

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PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Direct Submission

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 840;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

AF360860

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Molecular epidemiology of dengue type 2 virus in Venezuela:

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J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

21571640

PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Direct Submission

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 840;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

AF360860

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

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REFERENCE

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Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Direct Submission

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAACCGCG 28

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40 AATATGCTGAACCGCGAGAGAACCGCG 67

|||||

LOCUS

AF360860

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 840)

Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,

Holmes, E.C. and Gould, E.A.

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

21571640

PUBLISHED

11714970

Best Local Similarity	100.0%;	Pred. No. 0.13;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	AATATGCTGAAACGCGAGAGAAACCGCG	28					
Db	40	AATATGCTGAAACGCGAGAGAAACCGCG	67					
RESULT 4								
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DEFINITION		Dengue virus type 2 isolate LARD1910						polyprotein gene, partial cds.
ACCESSION		AF360862						
VERSION		AF360862.1						GI:18644125
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
MEDLINE								
PUBMED								
REFERENCE								
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TITLE								
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JOURNAL								
MEDLINE								
PUBMED					</			

Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.
 1 (bases 1 to 840)
 Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
 Holmes,E.C. and Gould,E.A.
 Molecular epidemiology of dengue type 2 virus in Venezuela:
 evidence for in situ virus evolution and recombination
 J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
 21571640 PUBMED
 11714970

2 (bases 1 to 840)
 Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
 Holmes,E.C. and Gould,E.A.
 Direct Submission
 Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
 Oxford OX2 6UD, England
 Location/Qualifiers
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 /mol_type="genomic RNA"
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 /country="Venezuela"
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ORIGIN
 Query Match 100.0%; Score 28; DB 14; Length 840;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATATGCTGAACCGCGAGAGAACC CGC 28
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 DB 40 AATATGCTGAACCGCGAGAGAACC CGC 67
 |||||

RESULT 6
 S66064
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 DEFINITION
 structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
 2319 nt].
 S66064
 S66064.1 GI:432575
 .
 Dengue virus type 4
 Dengue virus type 4
 Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.
 1 (bases 1 to 2319)
 Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
 Genetic determinants of dengue type 4 virus neurovirulence for mice
 J. Virol. 67 (11), 6567-6575 (1993)
 94016840
 8411360
 PUBMED

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED

REMARK
 GenBank staff at the National Library of Medicine created this
 entry [NCBI gi138430] from the original journal article.
 This sequence comes from Fig. 1.
 Location/Qualifiers
 1..2319
 /organism="Dengue virus type 4"
 /mol_type="genomic DNA"
 /db_xref="taxon:11070"

FEATURES
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ORIGIN

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Query Match 100.0%; Score 28; DB 14; Length 2319;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 7
AF469175
LOCUS
DEFINITION
Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION
AF469175
VERSION
AF469175.1 GI:18766554
KEYWORDS
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
TITLE
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
FEATURES
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/codon_start=1
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ORIGIN

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Query Match 100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
| | | | | | | | | | | | | | | | | |

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RESULT 8

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AF469176
LOCUS
DEFINITION
Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION
AF469176
VERSION
AF469176.1 GI:18766556
KEYWORDS
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
TITLE
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
FEATURES
source
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 9
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LOCUS
DEFINITION
Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION
AF509530
VERSION
AF509530.1 GI:21070436
KEYWORDS
Dengue virus type 2
SOURCE
ORGANISM
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
Ren.R., Yu.F., Dong.T., Wei.L., Hua.J., Yan.H. and Feng.C.
Isolation, identification and sequence analyses of dengue virus
type 2 strain GD19/2001
Unpublished
2 (bases 1 to 2325)
Ren.R., Yu.F., Dong.T., Wei.L., Hua.J., Yan.H. and Feng.C.
Direct Submission
TITLE
Submitted (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanhuang
Road, Guangzhou 510507, China
FEATURES
source
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/db_xref="GI:21070437"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 10
AY044442
LOCUS
DEFINITION
Dengue virus type 2 strain Mara3 polyprotein gene, partial cds.
ACCESSION
AY044442
VERSION
AY044442.1 GI:18643733
KEYWORDS
Dengue virus type 2
SOURCE
ORGANISM
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
Uzcategui.N.Y., Camacho.D., Comach.G., Cuello de Uzcategui.R.,
Holmes.E.C. and Gould.E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
2 (bases 1 to 2325)
Uzcategui.N.Y., Camacho.D., Comach.G., Cuello de Uzcategui.R.M.,
Holmes.E.C. and Gould.E.A.
Direct Submission
TITLE
Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
Road, Oxford OX1 3SR, United Kingdom
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0

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Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

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ORIGIN
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163

RESULT 14
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DEFINITION Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
PUBMED
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
CDS
FEATURES
source
1. .>2552
/organism="Dengue virus type 4"
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/isolate="D4.20 1998"
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/country="Puerto Rico"
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RAETWMSSEGAKHAQRVESWILRNPGFALLAGFMAYMIGQIGRTVFVLMMLVAP
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CDS
ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
    |||||
DB 37 AATATGCTGAACCGCGAGAGAAACCGCG 64

RESULT 15
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DEFINITION Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152040
VERSION AY152040.1 GI:28170815
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
PUBMED
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
CDS
FEATURES
source
1. .>2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.19 1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
/notes="acronym: DEN-4"
1. .>2552
/notes="contains core protein, matrix protein and envelope
glycoprotein"
/codon_start=1
/product="polyprotein precursor"
/protein_id="AAN38327.1"
/db_xref="GI:28170822"
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TVTYKCPLLVNTPEPIDDCNCLTSTWVMYGTCTOSGERRRERKRSVALTPHSGMGLET
RAETWMSSEGAKHAQRVESWILRNPGFALLAGFMAYMIGQIGRTVFVLMMLVAP
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LRTYCEASISNITTATRCPTGEPYLRKEEQQQYICRRDVRDVGNGCGFLFGKGV
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EVLKPDYBELTIDCEPRSGIDENEMILMKMKKTLWLHKQWFLDLPWTAGADTSEV
HNNKERMVTFKVPKARQDVTVLGSGEGMHSALAGATEVDSGDGNHMFAGHLKCKV
RNEKLRIKMSYTMCSGKFSIDKEMAEQHTGTVTVKVEGAGAPCKVPIERDVNKE
KVVGRIVSTPLAENTNSVNIIEPPFGDSYIVGVNSALTJLHFWRKSGSIGRMKFE
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LVLMIGTNSRNTSMATCIAGVGITLFLGFTVQADMGCVVWSGRELKCGSIGFVVDN
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CDS
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
    |||||
DB 37 AATATGCTGAACCGCGAGAGAAACCGCG 64
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Search completed: August 3, 2004, 19:08:57
Job time : 686.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 15:36:33 ; Search time 152.5 Seconds
(without alignments)
779.997 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aatattgctgaacgcgagagaaacccgcg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124039041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	100.0	28	ABX15698	Abx15698 Dengue vi
2	28	100.0	2357	ABX13740	Abx13740 Dengue vi
3	28	100.0	3381	AAT47666	Aat47666 Dengue vi
4	28	100.0	3381	AAX25114	Aax25114 Dengue vi
5	28	100.0	10616	AAD53912	Aad53912 Dengue vi
6	28	100.0	10648	AAD14612	Aad14612 Wild-type
7	28	100.0	10648	AAD14613	Aad14613 Attenuate
8	28	100.0	10649	AAD53911	Aad53911 Recombina
9	28	100.0	10649	AAD53910	Aad53910 Dengue vi
10	28	100.0	10717	AAD14605	Aad14605 Dengue vi
11	28	100.0	10723	AAQ12787	Aaq12787 Dengue 2
12	28	100.0	10723	AAT49303	Aat49303 cDNA enco
13	28	100.0	10723	AAT49304	Aat49304 cDNA enco
14	28	100.0	10723	AAD14614	Aad14614 Dengue vi
15	28	100.0	10723	AAD14607	Aad14607 Wild-type
16	28	100.0	10723	AAD14606	Aad14606 Dengue vi
17	28	100.0	10723	AAD14608	Aad14608 Attenuate
18	28	100.0	10756	AAD14609	Aad14609 Dengue vi
19	26.4	94.3	10718	AAQ51476	Aaq51476 DEN1-S275
20	26.4	94.3	10723	AAD14603	Aad14603 Dengue vi
21	26.4	94.3	10723	AAD14604	Aad14604 Dengue vi
22	26.4	94.3	10735	AAD14602	Aad14602 Attenuate
23	26.4	94.3	10735	AAD14601	Aad14601 Wild-type

24	26	92.9	26	3	AAC68744	Aac68744 Dengue vi
25	26	92.9	28	2	AAT75917	Aat75917 DEN-2 clo
26	24.8	88.6	10699	4	AAD14610	Aad14610 Wild-type
27	24.8	88.6	10699	4	AAD14611	Aad14611 Attenuate
28	22	78.6	72	6	AAF88836	Aaf88836 Green flu
c 29	19.2	68.6	1083	3	AAC44997	Aac44997 Arabidops
c 30	19	67.9	765	6	ABQ34003	Abq34003 Oligonuel
c 31	19	67.9	765	6	ABQ34002	Abq34002 Oligonuel
c 32	19	67.9	28564	9	ADD46068	Add46068 Human gen
c 33	18.8	67.1	1008	3	AAC46148	Aac46148 Arabidops
c 34	18.6	66.4	3002	4	ABL29849	AbL29849 Drosophil
c 35	18.6	66.4	7264	4	ABL29848	AbL29848 Drosophil
c 36	18.4	65.7	449	3	AA82355	Aa82355 N. mening
c 37	18.4	65.7	1443	3	AAC236361	Aac236361 DNA enco
c 38	18.4	65.7	1443	8	ABX16417	Abx16417 DNA enco
c 39	18.4	65.7	4512	2	AAQ22767	Aaq22767 JEV Nakay
c 40	18.4	65.7	10976	3	ABL50890	AbL50890 Japanese
c 41	18.4	65.7	12980	2	AAV59364	Aav59364 Hepatitis
c 42	18.4	65.7	12980	6	ABK87286	Abk87286 Hepatitis
c 43	18.4	65.7	12980	7	ACA62469	AcA62469 DNA enco
c 44	18.4	65.7	15065	3	AAZ36195	Aaz36195 Nucleotid
c 45	18.2	65.0	333	4	AAI81993	Aai81993 Human pol

ALIGNMENTS

RESULT 1
ABX15698
ID ABX15698 standard; DNA; 28 BP.
XX
AC ABX15698;
XX
DT 31-MAR-2003 (first entry)
XX
DE Dengue virus detection PCR primer #2.
XX
KW PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
KW dengue haemorrhagic fever; virus; viral detection.
XX
OS Dengue virus.
XX
PN US2002155435-A1.
XX
PD 24-OCT-2002.
XX
PF 28-FEB-2002; 2002US-00085944.
XX
PR 01-MAR-2001; 2001US-0272535P.
XX
(WANG/) WANG W.
XX
Wang W;
XX
DR WPI; 2003-182625/18.
XX
PT New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.
XX
XX Claim 28; Page 1; 6pp; English.
XX
XX This invention relates to novel Dengue virus reverse transcriptase (RT)
XX PCR primers which may be used to detect Dengue virus in a sample. Dengue
XX virus is a member of the flavivirus family and causes diseases including
XX dengue fever (DF) and dengue haemorrhagic fever. The invention also
XX comprises a method for detecting and quantitating dengue virus. The
XX dengue virus-specific primers of the invention are useful in reverse
XX transcriptase-polymerase chain reaction assays, particularly for
XX detecting or quantitating dengue virus in a sample. The present sequence
XX represents a dengue virus specific RT-PCR primer used in the method of
XX the invention

SQ Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAACCGCG 28
|||||
DB 1 AATATGCTGAACCGAGAGAAACCGCG 28

RESULT 2
ABX13740
ID ABX13740 standard; DNA; 2357 BP.
XX
AC ABX13740;
XX
DT 28-FEB-2003 (first entry)
XX
DE Dengue virus type 2 structural gene genome segment.

XX Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
KW PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
KW mosquito; Aedes aegyptii; acute undifferentiated fever;
KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
KW structural gene; virucide.

XX Dengue virus.

OS US6455509-B1.

PN 24-SEP-2002.

XX 04-JUN-1997; 97US-00869423.

XX 04-JUN-1996; 96US-0017839P.

XX (USNA) US SEC OF NAVY.

XX Kocheil TV, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;

XX WPI; 2003-066244/06.

XX New pharmaceutical compositions containing dengue nucleic acids, useful
PT as a vaccine, particularly for inducing a protective immune response in
PT mammalian subjects against the dengue virus infection.

XX Disclosure; Col 17-20; 26pp; English.

XX The invention discloses a pharmaceutical composition capable of inducing
CC an immune response in a mammalian subject, comprising an immunogenic
CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
CC which includes the envelope and membrane (preM) genes of a dengue type 1,
CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
CC the family Flaviviridae and is a positive strand RNA virus encoding ten
CC proteins. These genes are translated as a polypeptide which is cleaved by
CC host and viral proteinases. The virus envelope protein is a major antigen
CC which can be targeted by neutralising antibodies. The membrane protein
CC also appears on the virion surface and is required for proper processing
CC of the envelope protein. Dengue viruses are transmitted primarily by the
CC mosquito, Aedes aegyptii, and can lead to human illnesses ranging from
CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
CC dengue shock syndrome (DSS). Secondary infections, with a different
CC serotype, may lead to an immune enhancement phenomenon. The compositions
CC of the invention are DNA vaccines which are injected into the animal as a
CC technique of gene therapy. The composition is useful as a vaccine,
CC particularly for inducing a protective immune response in mammalian
CC subjects against the dengue virus infection. The sequence presented is
CC the dengue virus type 2 (Den 2) structural gene genome segment

XX Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 7; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAACCGCG 28
|||||
DB 60 AATATGCTGAACCGAGAGAAACCGCG 87

RESULT 3

AAT47666

ID AAT47666 standard; cDNA; 3381 BP.

XX AC AAT47666;

XX 17-OCT-2003 (revised)

DT 19-MAY-1997 (first entry)

XX Dengue virus serotype 2 PR159/S1 mutant sequence.

XX DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.

XX Dengue virus; serotype 2.

XX Key Location/Qualifiers

FT mutation /tag= a

FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
is GAA (Glu) in wild-type PR159"

FT mutation /tag= b

FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
is GTG (Val) in wild-type PR159"

FT mutation /tag= c

FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
is ATT (Ile) in wild-type PR159"

FT mutation /tag= d

FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-US007627.

XX 24-MAY-1995; 95US-00448734.

XX 07-JUN-1995; 95US-00488807.

XX 10-JUL-1995; 95US-00500469.

XX (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.

XX P-PSDB; AAW09409.

XX Sub:unit vaccine against flavivirus infection - contg. recombinant
PT envelope protein in secretable form, used for immunising against
PT flavivirus infection.

XX Example 1; Fig 3A-D; 121pp; English.

XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
CC conservation mutation in domain B of S1 that may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
CC the virus. The clone can be used to express recombinant secreted
CC polypeptides, comprising portions of the envelope protein (esp. domain B,
CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and

CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0094; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 40 AATATGCTGAACGCGAGAGAAACCGCG 67
|||||
RESULT 4
AAX25114
ID AAX25114 standard; cDNA; 3381 BP.
XX
AC AAX25114;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Dengue virus serotype 2 PR159/S1 viral capsid, prM, E, NS1 cDNA.
XX
KW Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
XX
OS Dengue virus; serotype 2.
XX
PN WO9906068-A2.
XX
PD 11-FEB-1999.
XX
PF 27-JUL-1998; 98WO-US015447.
XX
PR 31-JUL-1997; 97US-00904227.
XX
PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
PI Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
XX
WPI: 1999-153454/13.
DR P-PSDB; AAY05522.
XX
PT Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
PT 80%E protein, useful for protecting against flavivirus, especially dengue
PT virus infections.
XX
PS Example 1; Fig 3A-D; 60pp; English.
XX
CC This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
CC strain served as the source for DEN-2 genes used in the invention. A
CC vaccine for protecting against flavivirus infection comprises a dimeric
CC 80% E protein that has been secreted as a recombinant protein from a
CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
CC zipper domain through the homodimeric association of 2 leucine zipper
CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the
CC formation of a non-covalently associated four-helix bundle domain formed
CC upon association of two helix-turn-helix moieties attached to the C-
CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
CC efficiently secreted by recombinant cells, are easier to purify than
CC intracellular proteins, and generate a high titer neutralising antibody
CC response. The method is generally applicable to flaviviruses, in
CC particular dengue viruses such as DEN-2, where 80% E comprises amino
CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0094; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.0094; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 40 AATATGCTGAACGCGAGAGAAACCGCG 67
|||||
RESULT 5
AAD53912
ID AAD53912 standard; DNA; 10616 BP.
XX
AC AAD53912;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dengue virus type 2 strain rDEN2/4delta30 DNA.
XX
KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 97..10263
FT /tag= a
FT /product= "DEN4 strain rDEN2/4delta30 protein"
FT mat_peptide 97..438
FT /tag= c
FT /product= "Anchored capsid protein"
FT mat_peptide 97..396
FT /tag= b
FT /product= "Virion capsid protein"
FT mat_peptide 439..936
FT /tag= d
FT /product= "Membrane precursor protein"
FT mat_peptide 712..936
FT /tag= e
FT /product= "Membrane protein"
FT mat_peptide 937..2421
FT /tag= f
FT /product= "Envelope protein"
FT mat_peptide 2422..3477
FT /tag= g
FT /product= "NS1 protein"
FT mat_peptide 3478..4131
FT /tag= h
FT /product= "NS2A protein"
FT mat_peptide 4132..4521
FT /tag= i
FT /product= "NS2B protein"
FT mat_peptide 4522..6375
FT /tag= j
FT /product= "NS3 protein"
FT mat_peptide 6376..6756
FT /tag= k
FT /product= "NS4A protein"
FT mat_peptide 6757..6825
FT /tag= l
FT /product= "2K protein"
FT mat_peptide 6826..7560
FT /tag= m
FT /product= "NS4B protein"
FT mat_peptide 7561..10260
FT /tag= n
FT /product= "NS5 protein"
XX
PN WO200295075-A1.
XX
PD 28-NOV-2002.
XX
PF 22-MAY-2002; 2002WO-US016308.
XX
PR 22-MAY-2001; 2001US-0293049P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (BLAN/) BLANEY J E.
 XX
 PI Whitehead SS, Murphy BR, Hanley KA;
 XX
 XX WPI; 2003-120809/11.
 DR P-PSDB; AAE35314.
 XX
 XX New mutated flavivirus, useful for fine tuning the attenuation and growth
 PT characteristics of dengue virus vaccines for the prevention and/or
 PT treatment of dengue virus infection.
 XX
 XX Disclosure; Page 135-138; 246pp; English.
 XX
 XX The present invention relates to novel mutated flaviviruses comprising a
 CC phenotype in which the viral genome is modified by introduction of a
 CC mutation, singly or in combination, taken from mutations from recombinant
 CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
 CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
 CC dengue type 4 virus. The methods and compositions of the invention are
 CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain
 CC rDEN2/4delta30 DNA
 XX
 SQ Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 7; Length 10616;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
 RESULT 6
 AAD14612
 ID AAD14612 standard; cDNA; 10648 BP.
 AC AAD14612;
 XX
 XX 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 XX Wild-type, virulent DEN-4 1036 cDNA.
 DE
 XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
 KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
 KW
 XX Dengue virus; type IV.
 OS
 XX Key Location/Qualifiers
 FH 102..10265
 FT CDS /*tag= a
 FT /*product= "DEN-4 1036 protein"
 XX
 PN WO200160847-A2.
 XX
 XX 23-AUG-2001.
 PD
 XX 16-FEB-2001; 2001WO-US005142.
 PF
 XX 16-FEB-2000; 2000US-0182829P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Kinney RM, Kinney CYH, Buttrapet S, Gubler DL, Bhamarapravati N;
 XX
 PI WPI; 2001-497162/54.
 DR P-PSDB; AAE07991.
 XX

PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 PS Example 3; Page 373-389; 470pp; English.
 XX
 CC The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
 CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
 CC contains 5' non-coding region followed by a capsid protein (C) encoding
 CC region, premembrane/membrane protein (prM) encoding region, an envelope
 CC protein (E) encoding region, followed by the region encoding non-
 CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 4; Length 10648;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 Db 138 AATATGCTGAAACGCGAGAGAAACCGCG 165
 RESULT 7
 AAD14613
 ID AAD14613 standard; cDNA; 10648 BP.
 AC AAD14613;
 XX
 XX 01-NOV-2001 (first entry)
 DT
 XX
 XX Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
 DE
 XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX Dengue virus; type IV.
 OS
 XX Synthetic.
 XX Key Location/Qualifiers
 FH 102..10265
 FT CDS /*tag= a
 FT /*product= "DEN-4 PDK-48 protein variant"
 FT mutation replace(1211, T)
 FT /*tag= b
 FT mutation replace(1971, G)
 FT /*tag= c
 FT mutation replace(3182, G)
 FT /*tag= d
 FT mutation replace(6660, C)
 FT /*tag= e
 FT mutation replace(6957, A)
 FT /*tag= f
 FT mutation replace(7162, T)
 FT /*tag= g
 FT mutation replace(7546, C)
 FT /*tag= h
 FT mutation replace(7623, G)
 FT

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FT XX /*tag= i
PN WO200160847-A2.
PD XX
PP 23-AUG-2001.
PX XX
PY 16-FEB-2001; 2001WO-US005142.
PZ 16-FEB-2000; 2000US-0182829P.
QA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
QB Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;
QC WPI; 2001-497162/54.
QD P-PSDB; AAE07992.
QE Chimeric flaviviruses that are avirulent and immunogenic, useful for
  vaccinating against a range of dengue viruses.
QF Example 4; Page 397-413; 470pp; English.
QG The invention relates to avirulent, immunogenic flavivirus chimeras
  comprising amino acid mutations in the non-structural proteins of a
  flavivirus. Chimeric viruses containing the attenuation-mutated non-
  structural genes of the virus are used as a backbone into which the
  structural protein genes of a second flavivirus strain are inserted.
  These chimeric viruses elicit pronounced immunogenicity but lack the
  accompanying clinical symptoms of viral disease. Attenuated chimeric
  flaviviruses are combined in a pharmaceutical composition to confer
  simultaneous immunity against several strains of pathogenic flaviviruses
  such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
  flavivirus chimeras are also used as immunogens or multivalent vaccines
  to confer simultaneous protection against infections. The present cDNA
  sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
  used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
  to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
  contains 5' non-coding region followed by a capsid protein (C) encoding
  region, premembrane/membrane protein (prM) encoding region, an envelope
  protein (E) encoding region, followed by the region encoding non-
  structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
  non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
  48 times is designated as DEN-4 PDK-48 virus
XX SQ Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
  Query Match 100.0%; Score 28; DB 4; Length 10648;
  Best Local Similarity 100.0%; Pred. No. 0.011;
  Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
  |||||
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
  |||||
RESULT 8
ID AAD53911
XX AAD53911 standard; DNA; 10649 BP.
XX AC AAD53911;
XX DT 28-MAY-2003 (first entry)
XX DE Recombinant dengue virus type 4 strain rDEN4 DNA.
XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX OS Dengue virus.
XX FH Key Location/Qualifiers
FT CDS 102..10649
FT /*tag= a
FT /*product= "DEN4 strain rDEN4 protein"
```

```
FT mat_peptide 102..440
FT /*tag= c
FT /*product= "Anchored capsid protein"
FT mat_peptide 102..398
FT /*tag= b
FT /*product= "Virion capsid protein"
FT mat_peptide 441..938
FT /*tag= d
FT /*product= "Membrane precursor protein"
FT mat_peptide 714..938
FT /*tag= e
FT /*product= "Membrane protein"
FT mat_peptide 939..2423
FT /*tag= f
FT /*product= "Envelope protein"
FT mat_peptide 2424..3479
FT /*tag= g
FT /*product= "NS1 protein"
FT mat_peptide 3480..4133
FT /*tag= h
FT /*product= "NS2A protein"
FT mat_peptide 4134..4523
FT /*tag= i
FT /*product= "NS2B protein"
FT mat_peptide 4524..8377
FT /*tag= j
FT /*product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /*product= "NS4A protein"
FT mat_peptide 6638..7562
FT /*tag= m
FT /*product= "NS4B protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /*product= "2K protein"
FT mat_peptide 7563..10262
FT /*tag= n
FT /*product= "NS5 protein"
WO200295075-A1.
28-NOV-2002.
22-MAY-2002; 2002WO-US016308.
22-MAY-2001; 2001US-0293049P.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(BLAN/) BLANEY J E.
Whitehead SS, Murphy BR, Hanley KA;
WPI; 2003-120809/11.
P-PSDB; AAE35313.
New mutated flavivirus, useful for fine tuning the attenuation and growth
  characteristics of dengue virus vaccines for the prevention and/or
  treatment of dengue virus infection.
Disclosure; Page 131-132; 246pp; English.
The present invention relates to novel mutated flaviviruses comprising a
  phenotype in which the viral genome is modified by introduction of a
  mutation, singly or in combination, taken from mutations from recombinant
  virus bearing Vero adaptation mutations, putative Vero cell adaptation
  mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
  dengue type 4 virus. The methods and compositions of the invention are
  useful for fine tuning the attenuation and growth characteristics of
  dengue virus vaccines for the prevention and/or treatment of dengue virus
  infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
  Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
```

```
Query Match      100.0%; Score 28; DB 7; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACCGCGAGAGAAACCGCG 28
      |||||
Db      138 AATATGCTGAACCGCGAGAGAAACCGCG 165

RESULT 9
AAD53910
ID      AAD53910 standard; DNA; 10649 BP.
XX
AC      AAD53910;
XX
DT      28-MAY-2003 (first entry)
XX
DE      Dengue virus type 4 strain 2A DNA.
XX
KW      Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS      Dengue virus.
XX
FH      Key      Location/Qualifiers
CDS      102..10649
          /*tag= a
          /product= "DEN4 strain 2A protein"
FT      mat_peptide
          /*tag= c
          /product= "Anchored capsid protein"
FT      mat_peptide
          /*tag= b
          /product= "Virion capsid protein"
FT      mat_peptide
          /*tag= d
          /product= "Membrane precursor protein"
FT      mat_peptide
          /*tag= e
          /product= "Membrane protein"
FT      mat_peptide
          /*tag= f
          /product= "Envelope protein"
FT      mat_peptide
          /*tag= g
          /product= "NS1 protein"
FT      mat_peptide
          /*tag= h
          /product= "NS2A protein"
FT      mat_peptide
          /*tag= i
          /product= "NS2B protein"
FT      mat_peptide
          /*tag= j
          /product= "NS3 protein"
FT      mat_peptide
          /*tag= k
          /product= "NS4A protein"
FT      mat_peptide
          /*tag= l
          /product= "2K protein"
FT      mat_peptide
          /*tag= m
          /product= "NS4B protein"
FT      mat_peptide
          /*tag= n
          /product= "NS5 protein"
XX
WO200295075-A1.
XX
PN
PD
XX
PF      28-NOV-2002.
XX
PF      22-MAY-2002; 2002WO-US016308.

22-MAY-2001; 2001US-0293049P.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(BLANEY J E.
Whitehead SS, Murphy BR, Hanley KA;
WPI; 2003-120809/11.
P-PSDB; AAE35312.
XX
New mutated flavivirus, useful for fine tuning the attenuation and growth
characteristics of dengue virus vaccines for the prevention and/or
treatment of dengue virus infection.
XX
Disclosure; Page 123-126; 246pp; English.
XX
The present invention relates to novel mutated flaviviruses comprising a
phenotype in which the viral genome is modified by introduction of a
mutation, singly or in combination, taken from mutations from recombinant
virus bearing Vero adaptation mutations, putative Vero cell adaptation
mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
dengue type 4 virus. The methods and compositions of the invention are
useful for fine tuning the attenuation and growth characteristics of
dengue virus vaccines for the prevention and/or treatment of dengue virus
infection. The present sequence is Dengue virus type 4 strain 2A DNA
XX
SQ      Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 7; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACCGCGAGAGAAACCGCG 28
      |||||
Db      138 AATATGCTGAACCGCGAGAGAAACCGCG 165

RESULT 10
AAD14605
ID      AAD14605 standard; cDNA; 10717 BP.
XX
AC      AAD14605;
XX
DT      11-SEP-2003 (revised)
DT      01-NOV-2001 (first entry)
XX
DE      Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
XX
KW      Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS      Dengue virus; type II.
OS      Dengue virus; type III.
CHimeric.
FH      Key      Location/Qualifiers
CDS      97..10266
          /*tag= a
          /product= "DEN-2/3-VP1 fusion protein"
FT
FT
XX
WO200160847-A2.
XX
PN
XX
PD      23-AUG-2001.
XX
PF      16-FEB-2001; 2001WO-US005142.
XX
PR      16-FEB-2000; 2000US-0182829P.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX      Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
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DR WPI; 2001-497162/54.
DR P-PSDB; AAE07984.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 2; Page 203-219; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10717;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
RESULT 11
AAQ12787
ID AAQ12787 standard; RNA; 10723 BP.
AC AAQ12787;
XX
DT 25-MAR-2003 (revised)
DT 21-NOV-1991 (first entry)
XX
DE Dengue 2 virus genome.
XX
KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT FT /tag= a
FT mat_peptide 712..936
FT /tag= b
FT /product= "M protein"
FT mat_peptide 937..2421
FT /tag= c
FT /product= "E protein"
FT mat_peptide 2422..3477
FT /tag= d
FT /product= "NS1"
FT mat_peptide 3478..4131
FT /tag= e
FT /product= "NS2A"
FT mat_peptide 4132..4518
FT /tag= f
FT /product= "NS2B"
FT mat_peptide 4519..6375
FT /tag= g
FT /product= "NS3"

FT mat_peptide 6376..6825
FT /tag= h
FT /product= "NS4a"
FT mat_peptide 6826..7569
FT /tag= i
FT /product= "NS4B"
FT mat_peptide 7570..10269
FT /tag= j
FT /product= "NS5"
XX
XX FR2654113-A.
XX
XX 10-MAY-1991.
XX
XX 09-NOV-1989; 89FR-00914724.
XX
XX 09-NOV-1989; 89FR-00014724.
XX (INSP) INST PASTEUR.
XX
XX Vincent D;
XX
XX WPI: 1991-225002/31.
DR P-PSDB; AAR13166.
XX
PT Detection and identification of Flaviviridae in biological sample - by
PT amplifying consensus sequence then hybridisation opt. followed by typing,
PT e.g. sequencing amplified prod.
XX
PS Disclosure; Fig 3; 24pp; French.
XX
CC The dengue 2 virus is an example of a member of the Flaviviridae which
CC can be identified using the probe pair of the invention. A species-
CC specific sequence can be amplified using the claimed oligonucleotides as
CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
CC which can be identified include Japanese encephalitis virus and yellow
CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AAUAUGCUGAAACGCGAGAGAAACCGCG 163
RESULT 12
AAT49303
ID AAT49303 standard; cDNA; 10723 BP.
XX
AC AAT49303;
XX
DT 27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
XX
XX cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX
OS Dengue virus type 2 (strain 16681).
XX
XX Key Location/Qualifiers
FT CDS 97..10272
FT FT /tag= a
FT /product= "DEN-2 polyprotein
FT /transl_except (pos:9208..9210, aa:Xaa)"

```

FT XX /note= "Xaa = unknown amino acid"
PN WO9640933-A1.
XX 19-DEC-1996.
PD 06-JUN-1996; 96WO-US009209.
XX 07-JUN-1995; 95US-00483292.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX WPI; 1997-052330/05.
DR P-PSDB; AAW06590.
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX Claim 23; Page 107-121; 261pp; English.
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
CC -53, may be used in the production of a quadravalent vaccine which
CC provides immunity against all four serotypes of dengue virus. The vaccine
CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
CC protect against infection by all four serotypes of dengue virus, DEN-1,
CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
CC to produce the recombinant protein products of the DNA constructs which
CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGTAACGCGAGAGAAACCGCG 28
Db |||||
136 AATATGCTGTAACGCGAGAGAAACCGCG 163

RESULT 13
AAT49304
ID AAT49304 standard; cDNA; 10723 BP.
XX AC AAT49304;
XX 27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX Dengue virus type 2 (strain 16681).
OS Synthetic.
XX Key Location/Qualifiers
PH mutation 57
FT /tag= b
FT /note= "C>T mutation"

```

```

CDS
FT 97. .10272
FT /tag= a
FT /product= "DEN-2 attenuated polyprotein
FT /transl_except(pos:643. .645, aa:Xaa)
FT /transl_except(pos:1135. .1137, aa:Xaa)
FT /transl_except(pos:1393. .1395, aa:Xaa)
FT /transl_except(pos:2809. .2811, aa:Xaa)
FT /transl_except(pos:3040. .3042, aa:Xaa)
FT /transl_except(pos:9208. .9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
FT 524
FT mutation
FT /tag= c
FT /note= "A>T mutation, causes Asp to Val substitution"
FT 2055
FT mutation
FT /tag= d
FT /note= "C>T mutation"
FT 2579
FT mutation
FT /tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018
FT mutation
FT /tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547
FT mutation
FT /tag= g
FT /note= "C>T mutation"
FT 6599
FT mutation
FT /tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571
FT mutation
FT /tag= i
FT /note= "C>T mutation"
XX WO9640933-A1.
XX 19-DEC-1996.
XX 06-JUN-1996; 96WO-US009209.
XX 07-JUN-1995; 95US-00483292.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX WPI; 1997-052330/05.
DR P-PSDB; AAW06591.
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX Claim 27; Page 122-136; 261pp; English.
XX This sequence encodes the polyprotein from an attenuated derivative of
CC Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
CC polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
CC NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
CC production of a quadravalent vaccine which provides immunity against all
CC four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
CC -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
CC The new quadravalent vaccines are used to protect against infection by
CC all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
CC can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
CC syndrome (DHF/DSS). Host cells are used to produce the recombinant
CC protein products of the DNA constructs which are used in the vaccines.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.011;

```

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 14

AAD14614
ID AAD14614 standard; cDNA; 10723 BP.

XX AAD14614;

XX 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

XX

XX Dengue virus (DEN)-2/1-VP1 chimeric cDNA.

XX

XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX

XX Dengue virus; type I.

OS Dengue virus; type II.

XX

XX Key Location/Qualifiers

FT CDS 97..10272

FT /*tag= a

FT /product= "DEN-2/1-VP1 fusion protein"

XX

XX WO200160847-A2.

XX

XX 23-AUG-2001.

XX

XX 16-FEB-2001; 2001WO-US005142.

XX

XX 16-FEB-2000; 2000US-0182829P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;

XX

XX WPI; 2001-497162/54.

DR P-PSDB; AAE07993.

XX

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.

XX

XX Example 5; Page 422-438; 470pp; English.

XX

CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PPK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (ppM) and an envelope protein (E) from wild-
CC type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 28; DB 4; Length 10723;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 15

AAD14607

ID AAD14607 standard; cDNA; 10723 BP.

XX AAD14607;

XX

XX 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

XX

XX Wild-type, virulent DEN-2 16681 cDNA.

XX

XX Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.

XX

XX Dengue virus; type II.

XX

XX Key Location/Qualifiers

FT CDS 97..10272

FT /*tag= a

FT /product= "DEN-2 16681 protein"

XX

XX WO200160847-A2.

XX

XX 23-AUG-2001.

XX

XX 16-FEB-2001; 2001WO-US005142.

XX

XX 16-FEB-2000; 2000US-0182829P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;

XX

XX WPI; 2001-497162/54.

DR P-PSDB; AAE07986.

XX

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.

XX

XX Example 3; Page 252-268; 470pp; English.

XX

CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, pre-membrane/membrane protein (ppM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS2C-NS2D-NS2E-NS2F-NS2G-NS2H-NS2I-NS2J-NS2K-NS2L-NS2M-NS2N-NS2O-NS2P-NS2Q-NS2R-NS2S-NS2T-NS2U-NS2V-NS2W-NS2X-NS2Y-NS2Z-NS2AA-NS2AB-NS2AC-NS2AD-NS2AE-NS2AF-NS2AG-NS2AH-NS2AI-NS2AJ-NS2AK-NS2AL-NS2AM-NS2AN-NS2AO-NS2AP-NS2AQ-NS2AR-NS2AS-NS2AT-NS2AU-NS2AV-NS2AW-NS2AX-NS2AY-NS2AZ-NS2BA-NS2BB-NS2BC-NS2BD-NS2BE-NS2BF-NS2BG-NS2BH-NS2BI-NS2BJ-NS2BK-NS2BL-NS2BM-NS2BN-NS2BO-NS2BP-NS2BQ-NS2BR-NS2BS-NS2BT-NS2BU-NS2BV-NS2BW-NS2BX-NS2BY-NS2BZ-NS2CA-NS2CB-NS2CC-NS2CD-NS2CE-NS2CF-NS2CG-NS2CH-NS2CI-NS2CJ-NS2CK-NS2CL-NS2CM-NS2CN-NS2CO-NS2CP-NS2CQ-NS2CR-NS2CS-NS2CT-NS2CU-NS2CV-NS2CW-NS2CX-NS2CY-NS2CZ-NS2DA-NS2DB-NS2DC-NS2DD-NS2DE-NS2DF-NS2DG-NS2DH-NS2DI-NS2DJ-NS2DK-NS2DL-NS2DM-NS2DN-NS2DO-NS2DP-NS2DQ-NS2DR-NS2DS-NS2DT-NS2DU-NS2DV-NS2DW-NS2DX-NS2DY-NS2DZ-NS2EA-NS2EB-NS2EC-NS2ED-NS2EE-NS2EF-NS2EG-NS2EH-NS2EI-NS2EJ-NS2EK-NS2EL-NS2EM-NS2EN-NS2EO-NS2EP-NS2EQ-NS2ER-NS2ES-NS2ET-NS2EU-NS2EV-NS2EW-NS2EX-NS2EY-NS2EZ-NS2FA-NS2FB-NS2FC-NS2FD-NS2FE-NS2FF-NS2FG-NS2FH-NS2FI-NS2FJ-NS2FK-NS2FL-NS2FM-NS2FN-NS2FO-NS2FP-NS2FQ-NS2FR-NS2FS-NS2FT-NS2FU-NS2FV-NS2FW-NS2FX-NS2FY-NS2FZ-NS2GA-NS2GB-NS2GC-NS2GD-NS2GE-NS2GF-NS2GG-NS2GH-NS2GI-NS2GJ-NS2GK-NS2GL-NS2GM-NS2GN-NS2GO-NS2GP-NS2GQ-NS2GR-NS2GS-NS2GT-NS2GU-NS2GV-NS2GW-NS2GX-NS2GY-NS2GZ-NS2HA-NS2HB-NS2HC-NS2HD-NS2HE-NS2HF-NS2HG-NS2HH-NS2HI-NS2HJ-NS2HK-NS2HL-NS2HM-NS2HN-NS2HO-NS2HP-NS2HQ-NS2HR-NS2HS-NS2HT-NS2HU-NS2HV-NS2HW-NS2HX-NS2HY-NS2HZ-NS2IA-NS2IB-NS2IC-NS2ID-NS2IE-NS2IF-NS2IG-NS2IH-NS2II-NS2IJ-NS2IK-NS2IL-NS2IM-NS2IN-NS2IO-NS2IP-NS2IQ-NS2IR-NS2IS-NS2IT-NS2IU-NS2IV-NS2IW-NS2IX-NS2IY-NS2IZ-NS2JA-NS2JB-NS2JC-NS2JD-NS2JE-NS2JF-NS2JG-NS2JH-NS2JI-NS2JJ-NS2JK-NS2JL-NS2JM-NS2JN-NS2JO-NS2JP-NS2JQ-NS2JR-NS2JS-NS2JT-NS2JU-NS2JV-NS2JW-NS2JX-NS2JY-NS2JZ-NS2KA-NS2KB-NS2KC-NS2KD-NS2KE-NS2KF-NS2KG-NS2KH-NS2KI-NS2KJ-NS2KK-NS2KL-NS2KM-NS2KN-NS2KO-NS2KP-NS2KQ-NS2KR-NS2KS-NS2KT-NS2KU-NS2KV-NS2KW-NS2KX-NS2KY-NS2KZ-NS2LA-NS2LB-NS2LC-NS2LD-NS2LE-NS2LF-NS2LG-NS2LH-NS2LI-NS2LJ-NS2LK-NS2LL-NS2LM-NS2LN-NS2LO-NS2LP-NS2LQ-NS2LR-NS2LS-NS2LT-NS2LU-NS2LV-NS2LW-NS2LX-NS2LY-NS2LZ-NS2MA-NS2MB-NS2MC-NS2MD-NS2ME-NS2MF-NS2MG-NS2MH-NS2MI-NS2MJ-NS2MK-NS2ML-NS2MM-NS2MN-NS2MO-NS2MP-NS2MQ-NS2MR-NS2MS-NS2MT-NS2MU-NS2MV-NS2MW-NS2MX-NS2MY-NS2MZ-NS2NA-NS2NB-NS2NC-NS2ND-NS2NE-NS2NF-NS2NG-NS2NH-NS2NI-NS2NJ-NS2NK-NS2NL-NS2NM-NS2NO-NS2NP-NS2NQ-NS2NR-NS2NS-NS2NT-NS2NU-NS2NV-NS2NW-NS2NX-NS2NY-NS2NZ-NS2OA-NS2OB-NS2OC-NS2OD-NS2OE-NS2OF-NS2OG-NS2OH-NS2OI-NS2OJ-NS2OK-NS2OL-NS2OM-NS2ON-NS2OO-NS2OP-NS2OQ-NS2OR-NS2OS-NS2OT-NS2OU-NS2OV-NS2OW-NS2OX-NS2OY-NS2OZ-NS2PA-NS2PB-NS2PC-NS2PD-NS2PE-NS2PF-NS2PG-NS2PH-NS2PI-NS2PJ-NS2PK-NS2PL-NS2PM-NS2PN-NS2PO-NS2PP-NS2PQ-NS2PR-NS2PS-NS2PT-NS2PU-NS2PV-NS2PW-NS2PX-NS2PY-NS2PZ-NS2QA-NS2QB-NS2QC-NS2QD-NS2QE-NS2QF-NS2QG-NS2QH-NS2QI-NS2QJ-NS2QK-NS2QL-NS2QM-NS2QN-NS2QO-NS2QP-NS2QQ-NS2QR-NS2QS-NS2QT-NS2QU-NS2QV-NS2QW-NS2QX-NS2QY-NS2QZ-NS2RA-NS2RB-NS2RC-NS2RD-NS2RE-NS2RF-NS2RG-NS2RH-NS2RI-NS2RJ-NS2RK-NS2RL-NS2RM-NS2RN-NS2RO-NS2RP-NS2RQ-NS2RR-NS2RS-NS2RT-NS2RU-NS2RV-NS2RW-NS2RX-NS2RY-NS2RZ-NS2SA-NS2SB-NS2SC-NS2SD-NS2SE-NS2SF-NS2SG-NS2SH-NS2SI-NS2SJ-NS2SK-NS2SL-NS2SM-NS2SN-NS2SO-NS2SP-NS2SQ-NS2SR-NS2SS-NS2ST-NS2SU-NS2SV-NS2SW-NS2SX-NS2SY-NS2SZ-NS2TA-NS2TB-NS2TC-NS2TD-NS2TE-NS2TF-NS2TG-NS2TH-NS2TI-NS2TJ-NS2TK-NS2TL-NS2TM-NS2TN-NS2TO-NS2TP-NS2TQ-NS2TR-NS2TS-NS2TT-NS2TU-NS2TV-NS2TW-NS2TX-NS2TY-NS2TZ-NS2UA-NS2UB-NS2UC-NS2UD-NS2UE-NS2UF-NS2UG-NS2UH-NS2UI-NS2UJ-NS2UK-NS2UL-NS2UM-NS2UN-NS2UO-NS2UP-NS2UQ-NS2UR-NS2US-NS2UT-NS2UU-NS2UV-NS2UW-NS2UX-NS2UY-NS2UZ-NS2VA-NS2VB-NS2VC-NS2VD-NS2VE-NS2VF-NS2VG-NS2VH-NS2VI-NS2VJ-NS2VK-NS2VL-NS2VM-NS2VN-NS2VO-NS2VP-NS2VQ-NS2VR-NS2VS-NS2VT-NS2VU-NS2VV-NS2VW-NS2VX-NS2VY-NS2VZ-NS2WA-NS2WB-NS2WC-NS2WD-NS2WE-NS2WF-NS2WG-NS2WH-NS2WI-NS2WJ-NS2WK-NS2WL-NS2WM-NS2WN-NS2WO-NS2WP-NS2WQ-NS2WR-NS2WS-NS2WT-NS2WU-NS2WV-NS2WW-NS2WX-NS2WY-NS2WZ-NS2XA-NS2XB-NS2XC-NS2XD-NS2XE-NS2XF-NS2XG-NS2XH-NS2XI-NS2XJ-NS2XK-NS2XL-NS2XM-NS2XN-NS2XO-NS2XP-NS2XQ-NS2XR-NS2XS-NS2XT-NS2XU-NS2XV-NS2XW-NS2XX-NS2XY-NS2XZ-NS2YA-NS2YB-NS2YC-NS2YD-NS2YE-NS2YF-NS2YG-NS2YH-NS2YI-NS2YJ-NS2YK-NS2YL-NS2YM-NS2YN-NS2YO-NS2YP-NS2YQ-NS2YR-NS2YS-NS2YT-NS2YU-NS2YV-NS2YW-NS2YX-NS2YY-NS2YZ-NS2ZA-NS2ZB-NS2ZC-NS2ZD-NS2ZE-NS2ZF-NS2ZG-NS2ZH-NS2ZI-NS2ZJ-NS2ZK-NS2ZL-NS2ZM-NS2ZN-NS2ZO-NS2ZP-NS2ZQ-NS2ZR-NS2ZS-NS2ZT-NS2ZU-NS2ZV-NS2ZW-NS2ZX-NS2ZY-NS2ZZ-NS2AA-NS2AB-NS2AC-NS2AD-NS2AE-NS2AF-NS2AG-NS2AH-NS2AI-NS2AJ-NS2AK-NS2AL-NS2AM-NS2AN-NS2AO-NS2AP-NS2AQ-NS2AR-NS2AS-NS2AT-NS2AU-NS2AV-NS2AW-NS2AX-NS2AY-NS2AZ-NS2BA-NS2BB-NS2BC-NS2BD-NS2BE-NS2BF-NS2BG-NS2BH-NS2BI-NS2BJ-NS2BK-NS2BL-NS2BM-NS2BN-NS2BO-NS2BP-NS2BQ-NS2BR-NS2BS-NS2BT-NS2BU-NS2BV-NS2BW-NS2BX-NS2BY-NS2BZ-NS2CA-NS2CB-NS2CC-NS2CD-NS2CE-NS2CF-NS2CG-NS2CH-NS2CI-NS2CJ-NS2CK-NS2CL-NS2CM-NS2CN-NS2CO-NS2CP-NS2CQ-NS2CR-NS2CS-NS2CT-NS2CU-NS2CV-NS2CW-NS2CX-NS2CY-NS2CZ-NS2DA-NS2DB-NS2DC-NS2DD-NS2DE-NS2DF-NS2DG-NS2DH-NS2DI-NS2DJ-NS2DK-NS2DL-NS2DM-NS2DN-NS2DO-NS2DP-NS2DQ-NS2DR-NS2DS-NS2DT-NS2DU-NS2DV-NS2DW-NS2DX-NS2DY-NS2DZ-NS2EA-NS2EB-NS2EC-NS2ED-NS2EE-NS2EF-NS2EG-NS2EH-NS2EI-NS2EJ-NS2EK-NS2EL-NS2EM-NS2EN-NS2EO-NS2EP-NS2EQ-NS2ER-NS2ES-NS2ET-NS2EU-NS2EV-NS2EW-NS2EX-NS2EY-NS2EZ-NS2FA-NS2FB-NS2FC-NS2FD-NS2FE-NS2FF-NS2FG-NS2FH-NS2FI-NS2FJ-NS2FK-NS2FL-NS2FM-NS2FN-NS2FO-NS2FP-NS2FQ-NS2FR-NS2FS-NS2FT-NS2FU-NS2FV-NS2FW-NS2FX-NS2FY-NS2FZ-NS2GA-NS2GB-NS2GC-NS2GD-NS2GE-NS2GF-NS2GG-NS2GH-NS2GI-NS2GJ-NS2GK-NS2GL-NS2GM-NS2GN-NS2GO-NS2GP-NS2GQ-NS2GR-NS2GS-NS2GT-NS2GU-NS2GV-NS2GW-NS2GX-NS2GY-NS2GZ-NS2HA-NS2HB-NS2HC-NS2HD-NS2HE-NS2HF-NS2HG-NS2HH-NS2HI-NS2HJ-NS2HK-NS2HL-NS2HM-NS2HN-NS2HO-NS2HP-NS2HQ-NS2HR-NS2HS-NS2HT-NS2HU-NS2HV-NS2HW-NS2HX-NS2HY-NS2HZ-NS2IA-NS2IB-NS2IC-NS2ID-NS2IE-NS2IF-NS2IG-NS2IH-NS2II-NS2IJ-NS2IK-NS2IL-NS2IM-NS2IN-NS2IO-NS2IP-NS2IQ-NS2IR-NS2IS-NS2IT-NS2IU-NS2IV-NS2IW-NS2IX-NS2IY-NS2IZ-NS2JA-NS2JB-NS2JC-NS2JD-NS2JE-NS2JF-NS2JG-NS2JH-NS2JI-NS2JJ-NS2JK-NS2JL-NS2JM-NS2JN-NS2JO-NS2JP-NS2JQ-NS2JR-NS2JS-NS2JT-NS2JU-NS2JV-NS2JW-NS2JX-NS2JY-NS2JZ-NS2KA-NS2KB-NS2KC-NS2KD-NS2KE-NS2KF-NS2KG-NS2KH-NS2KI-NS2KJ-NS2KK-NS2KL-NS2KM-NS2KN-NS2KO-NS2KP-NS2KQ-NS2KR-NS2KS-NS2KT-NS2KU-NS2KV-NS2KW-NS2KX-NS2KY-NS2KZ-NS2LA-NS2LB-NS2LC-NS2LD-NS2LE-NS2LF-NS2LG-NS2LH-NS2LI-NS2LJ-NS2LK-NS2LM-NS2LN-NS2LO-NS2LP-NS2LQ-NS2LR-NS2LS-NS2LT-NS2LU-NS2LV-NS2LW-NS2LX-NS2LY-NS2LZ-NS2MA-NS2MB-NS2MC-NS2MD-NS2ME-NS2MF-NS2MG-NS2MH-NS2MI-NS2MJ-NS2MK-NS2ML-NS2MM-NS2MN-NS2MO-NS2MP-NS2MQ-NS2MR-NS2MS-NS2MT-NS2MU-NS2MV-NS2MW-NS2MX-NS2MY-NS2MZ-NS2NA-NS2NB-NS2NC-NS2ND-NS2NE-NS2NF-NS2NG-NS2NH-NS2NI-NS2NJ-NS2NK-NS2NL-NS2NM-NS2NO-NS2NP-NS2NQ-NS2NR-NS2NS-NS2NT-NS2NU-NS2NV-NS2NW-NS2NX-NS2NY-NS2NZ-NS2OA-NS2OB-NS2OC-NS2OD-NS2OE-NS2OF-NS2OG-NS2OH-NS2OI-NS2OJ-NS2OK-NS2OL-NS2OM-NS2ON-NS2OO-NS2OP-NS2OQ-NS2OR-NS2OS-NS2OT-NS2OU-NS2OV-NS2OW-NS2OX-NS2OY-NS2OZ-NS2PA-NS2PB-NS2PC-NS2PD-NS2PE-NS2PF-NS2PG-NS2PH-NS2PI-NS2PJ-NS2PK-NS2PL-NS2PM-NS2PN-NS2PO-NS2PP-NS2PQ-NS2PR-NS2PS-NS2PT-NS2PU-NS2PV-NS2PW-NS2PX-NS2PY-NS2PZ-NS2QA-NS2QB-NS2QC-NS2QD-NS2QE-NS2QF-NS2QG-NS2QH-NS2QI-NS2QJ-NS2QK-NS2QL-NS2QM-NS2QN-NS2QO-NS2QP-NS2QQ-NS2QR-NS2QS-NS2QT-NS2QU-NS2QV-NS2QW-NS2QX-NS2QY-NS2QZ-NS2RA-NS2RB-NS2RC-NS2RD-NS2RE-NS2RF-NS2RG-NS2RH-NS2RI-NS2RJ-NS2RK-NS2RL-NS2RM-NS2RN-NS2RO-NS2RP-NS2RQ-NS2RR-NS2RS-NS2RT-NS2RU-NS2RV-NS2RW-NS2RX-NS2RY-NS2RZ-NS2SA-NS2SB-NS2SC-NS2SD-NS2SE-NS2SF-NS2SG-NS2SH-NS2SI-NS2SJ-NS2SK-NS2SL-NS2SM-NS2SN-NS2SO-NS2SP-NS2SQ-NS2SR-NS2SS-NS2ST-NS2SU-NS2SV-NS2SW-NS2SX-NS2SY-NS2SZ-NS2TA-NS2TB-NS2TC-NS2TD-NS2TE-NS2TF-NS2TG-NS2TH-NS2TI-NS2TJ-NS2TK-NS2TL-NS2TM-NS2TN-NS2TO-NS2TP-NS2TQ-NS2TR-NS2TS-NS2TT-NS2TU-NS2TV-NS2TW-NS2TX-NS2TY-NS2TZ-NS2UA-NS2UB-NS2UC-NS2UD-NS2UE-NS2UF-NS2UG-NS2UH-NS2UI-NS2UJ-NS2UK-NS2UL-NS2UM-NS2UN-NS2UO-NS2UP-NS2UQ-NS2UR-NS2US-NS2UT-NS2UU-NS2UV-NS2UW-NS2UX-NS2UY-NS2UZ-NS2VA-NS2VB-NS2VC-NS2VD-NS2VE-NS2VF-NS2VG-NS2VH-NS2VI-NS2VJ-NS2VK-NS2VL-NS2VM-NS2VN-NS2VO-NS2VP-NS2VQ-NS2VR-NS2VS-NS2VT-NS2VU-NS2VV-NS2VW-NS2VX-NS2VY-NS2VZ-NS2WA-NS2WB-NS2WC-NS2WD-NS2WE-NS2WF-NS2WG-NS2WH-NS2WI-NS2WJ-NS2WK-NS2WL-NS2WM-NS2WN-NS2WO-NS2WP-NS2WQ-NS2WR-NS2WS-NS2WT-NS2WU-NS2WV-NS2WW-NS2WX-NS2WY-NS2WZ-NS2XA-NS2XB-NS2XC-NS2XD-NS2XE-NS2XF-NS2XG-NS2XH-NS2XI-NS2XJ-NS2XK-NS2XL-NS2XM-NS2XN-NS2XO-NS2XP-NS2XQ-NS2XR-NS2XS-NS2XT-NS2XU-NS2XV-NS2XW-NS2XX-NS2XY-NS2XZ-NS2YA-NS2YB-NS2YC-NS2YD-NS2YE-NS2YF-NS2YG-NS2YH-NS2YI-NS2YJ-NS2YK-NS2YL-NS2YM-NS2YN-NS2YO-NS2YP-NS2YQ-NS2YR-NS2YS-NS2YT-NS2YU-NS2YV-NS2YW-NS2YX-NS2YY-NS2YZ-NS2ZA-NS2ZB-NS2ZC-NS2ZD-NS2ZE-NS2ZF-NS2ZG-NS2ZH-NS2ZI-NS2ZJ-NS2ZK-NS2ZL-NS2ZM-NS2ZN-NS2ZO-NS2ZP-NS2ZQ-NS2ZR-NS2ZS-NS2ZT-NS2ZU-NS2ZV-NS2ZW-NS2ZX-NS2ZY-NS2ZZ-NS2AA-NS2AB-NS2AC-NS2AD-NS2AE-NS2AF-NS2AG-NS2AH-NS2AI-NS2AJ-NS2AK-NS2AL-NS2AM-NS2AN-NS2AO-NS2AP-NS2AQ-NS2AR-NS2AS-NS2AT-NS2AU-NS2AV-NS2AW-NS2AX-NS2AY-NS2AZ-NS2BA-NS2BB-NS2BC-NS2BD-NS2BE-NS2BF-NS2BG-NS2BH-NS2BI-NS2BJ-NS2BK-NS2BL-NS2BM-NS2BN-NS2BO-NS2BP-NS2BQ-NS2BR-NS2BS-NS2BT-NS2BU-NS2BV-NS2BW-NS2BX-NS2BY-NS2BZ-NS2CA-NS2CB-NS2CC-NS2CD-NS2CE-NS2CF-NS2CG-NS2CH-NS2CI-NS2CJ-NS2CK-NS2CL-NS2CM-NS2CN-NS2CO-NS2CP-NS2CQ-NS2CR-NS2CS-NS2CT-NS2CU-NS2CV-NS2CW-NS2CX-NS2CY-NS2CZ-NS2DA-NS2DB-NS2DC-NS2DD-NS2DE-NS2DF-NS2DG-NS2DH-NS2DI-NS2DJ-NS2DK-NS2DL-NS2DM-NS2DN-NS2DO-NS2DP-NS2DQ-NS2DR-NS2DS-NS2DT-NS2DU-NS2DV-NS2DW-NS2DX-NS2DY-NS2DZ-NS2EA-NS2EB-NS2EC-NS2ED-NS2EE-NS2EF-NS2EG-NS2EH-NS2EI-NS2EJ-NS2EK-NS2EL-NS2EM-NS2EN-NS2EO-NS2EP-NS2EQ-NS2ER-NS2ES-NS2ET-NS2EU-NS2EV-NS2EW-NS2EX-NS2EY-NS2EZ-NS2FA-NS2FB-NS2FC-NS2FD-NS2FE-NS2FF-NS2FG-NS2FH-NS2FI-NS2FJ-NS2FK-NS2FL-NS2FM-NS2FN-NS2FO-NS2FP-NS2FQ-NS2FR-NS2FS-NS2FT-NS2FU-NS2FV-NS2FW-NS2FX-NS2FY-NS2FZ-NS2GA-NS2GB-NS2GC-NS2GD-NS2GE-NS2GF-NS2GG-NS2GH-NS2GI-NS2GJ-NS2GK-NS2GL-NS2GM-NS2GN-NS2GO-NS2GP-NS2GQ-NS2GR-NS2GS-NS2GT-NS2GU-NS2GV-NS2GW-NS2GX-NS2GY-NS2GZ-NS2HA-NS2HB-NS2HC-NS2HD-NS2HE-NS2HF-NS2HG-NS2HH-NS2HI-NS2HJ-NS2HK-NS2HL-NS2HM-NS2HN-NS2HO-NS2HP-NS2HQ-NS2HR-NS2HS-NS2HT-NS2HU-NS2HV-NS2HW-NS2HX-NS2HY-NS2HZ-NS2IA-NS2IB-NS2IC-NS2ID-NS2IE-NS2IF-NS2IG-NS2IH-NS2II-NS2IJ-NS2IK-NS2IL-NS2IM-NS2IN-NS2IO-NS2IP-NS2IQ-NS2IR-NS2IS-NS2IT-NS2IU-NS2IV-NS2IW-NS2IX-NS2IY-NS2IZ-NS2JA-NS2JB-NS2JC-NS2JD-NS2JE-NS2JF-NS2JG-NS2JH-NS2JI-NS2JJ-NS2JK-NS2JL-NS2JM-NS2JN-NS2JO-NS2JP-NS2JQ-NS2JR-NS2JS-NS2JT-NS2JU-NS2JV-NS2JW-NS2JX-NS2JY-NS2JZ-NS2KA-NS2KB-NS2KC-NS2KD-NS2KE-NS2KF-NS2KG-NS2KH-NS2KI-NS2KJ-NS2KK-NS2KL-NS2KM-NS2KN-NS2KO-NS2KP-NS2KQ-NS2KR-NS2KS-NS2KT-NS2KU-NS2KV-NS2KW-NS2KX-NS2KY-NS2KZ-NS2LA-NS2LB-NS2LC-NS2LD-NS2LE-NS2LF-NS2LG-NS2LH-NS2LI-NS2LJ-NS2LK-NS2LM-NS2LN-NS2LO-NS2LP-NS2LQ-NS2LR-NS2LS-NS2LT-NS2LU-NS2LV-NS2LW-NS2LX-NS2LY-NS2LZ-NS2MA-NS2MB-NS2MC-NS2MD-NS2ME-NS2MF-NS2MG-NS2MH-NS2MI-NS2MJ-NS2MK-NS2ML-NS2MM-NS2MN-NS2MO-NS2MP-NS2MQ-NS2MR-NS2MS-NS2MT-NS2MU-NS2MV-NS2MW-NS2MX-NS2MY-NS2MZ-NS2NA-NS2NB-NS2NC-NS2ND-NS2NE-NS2NF-NS2NG-NS2NH-NS2NI-NS2NJ-NS2NK-NS2NL-NS2NM-NS2NO-NS2NP-NS2NQ-NS2NR-NS2NS-NS2NT-NS2NU-NS2NV-NS2NW-NS2NX-NS2NY-NS2NZ-NS2OA-NS2OB-NS2OC-NS2OD-NS2OE-NS2OF-NS2OG-NS2OH-NS2OI-NS2OJ-NS2OK-NS2OL-NS2OM-NS2ON-NS2OO-NS2OP-NS2OQ-NS2OR-NS2OS-NS2OT-NS2OU-NS2OV-NS2OW-NS2OX-NS2OY-NS2OZ-NS2PA-NS2PB-NS2PC-NS2PD-NS2PE-NS2PF-NS2PG-NS2PH-NS2PI-NS2PJ-NS2PK-NS2PL-NS2PM-NS2PN-NS2PO-NS2PP-NS2PQ-NS2PR-NS2PS-NS2PT-NS2PU-NS2PV-NS2PW-NS2PX-NS2PY-NS2PZ-NS2QA-NS2QB-NS2QC-NS2QD-NS2QE-NS2QF-NS2QG-NS2QH-NS2QI-NS2QJ-NS2QK-NS2QL-NS2QM-NS2QN-NS2QO-NS2QP-NS2QQ-NS2QR-NS2QS-NS2QT-NS2QU-NS2QV-NS2QW-NS2QX-NS2QY-NS2QZ-NS2RA-NS2RB-NS2RC-NS2RD-NS2RE-NS2RF-NS2RG-NS2RH-NS2RI-NS2RJ-NS2RK-NS2RL-NS2RM-NS2RN-NS2RO-NS2RP-NS2RQ-NS2RR-NS2RS-NS2RT-NS2RU-NS2RV-NS2RW-NS2RX-NS2RY-NS2RZ-NS2SA-NS2SB-NS2SC-NS2SD-NS2SE-NS2SF-NS2SG-NS2SH-NS2SI-NS2SJ-NS2SK-NS2SL-NS2SM-NS2SN-NS2SO-NS2SP-NS2SQ-NS2SR-NS2SS-NS2ST-NS2SU-NS2SV-NS2SW-NS2SX-NS2SY-NS2SZ-NS2TA-NS2TB-NS2TC-NS2TD-NS2TE-NS2TF-NS2TG-NS2TH-NS2TI-NS2TJ-NS2TK-NS2TL-NS2TM-NS2TN-NS2TO-NS2TP-

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:
2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	28	100.0	2357	4	US-08-869-423-1
2	28	100.0	3381	3	US-08-937-195-1
3	28	100.0	3381	3	US-08-937-195-2
4	28	100.0	3381	3	US-08-915-152-1
5	28	100.0	3381	3	US-08-915-152-2
6	28	100.0	3381	5	PCT-US96-07627-1
7	28	100.0	3381	5	PCT-US96-07627-2
8	26.4	94.3	10718	3	US-08-325-426B-1
9	18.4	65.7	1443	3	US-09-078-173A-11
10	18.4	65.7	4512	1	US-08-224-391-52
11	18.4	65.7	4512	3	US-08-484-304-52
12	18.4	65.7	12980	1	US-08-911-566-5
13	18.4	65.7	12980	3	US-09-034-756-5
14	17.4	62.1	993	3	US-08-875-233-11
15	17.4	62.1	1227	4	US-09-328-352-1888
16	17.4	62.1	2646	4	US-09-221-017B-558
17	17.4	62.1	5026	4	US-09-549-872B-5
18	17.4	62.1	6612	4	US-09-549-872B-5
19	17.4	62.1	11207	4	US-09-549-872B-2
20	17.2	61.4	3243	1	US-08-611-107-32
21	17.2	61.4	24358	4	US-09-392-812A-1
22	17	60.7	435	4	US-09-252-991A-1169
23	17	60.7	2355	4	US-08-913-159-12
24	17	60.7	2409	4	US-09-252-991A-1259
25	17	60.7	3378	4	US-09-328-352-4107
26	16.8	60.0	287	4	US-09-313-294A-1156
27	16.8	60.0	936	4	US-09-252-991A-11497

ALIGNMENTS

RESULT 1

US-08-869-423-1

; Sequence 1, Application US/08869423

; Patent No. 6455509

; GENERAL INFORMATION:

; APPLICANT: Kochel, Tadeusz

; APPLICANT: Porter, Kevin R.

; APPLICANT: Raviprakash, Kanakatte

; APPLICANT: Hoffmann, Stephen L.

; APPLICANT: Hayes, Curtis G.

; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce

; TITLE OF INVENTION: Neutralizing Antibodies

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Naval Medical Res. & Dev. Cmd.

; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12

; CITY: Bethesda

; STATE: Maryland

; COUNTRY: U.S.A.

; ZIP: 20889-5606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/869,423

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/017,839

; FILING DATE: 04-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Kalish, Daniel

; REGISTRATION NUMBER: 33,599

; REFERENCE/DOCKET NUMBER: NC 77,654

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 295-5642

; TELEFAX: (301) 295-1022

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: RNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

Sequence 6977, Ap
Sequence 522, App
Sequence 314, App
Sequence 295, App
Sequence 361, App
Sequence 214, App
Sequence 34, Appli
Sequence 105, App
Sequence 710, App
Sequence 9, Appli
Sequence 158, App
Sequence 450, App
Sequence 450, App
Sequence 450, App
Sequence 693, App
Sequence 17, Appli
Sequence 1, Appli

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/ ORGANISM: Dengue virus
/ STRAIN: New Guinea C
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: Prem and Envelope
/ MAP POSITION: 330-2446
/ UNITS: bp
/ PUBLICATION INFORMATION:
/ AUTHORS: Gruenberg, A
/ AUTHORS: Woo, W S
/ AUTHORS: Biedrzycka, A
/ AUTHORS: Wright, P J
/ TITLE: Partial nucleotide sequence and deduced amino
/ TITLE: acid sequence of the structural proteins of dengue
/ TITLE: virus type 2, New Guinea C and PUO-218 strains
/ JOURNAL: J. Gen. Virol.
/ VOLUME: 69
/ PAGES: 1391-1398
/ DATE: 1988
/ PUBLICATION INFORMATION:
/ AUTHORS: Irie, K
/ AUTHORS: Mohan, P M
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Putnak, R
/ AUTHORS: Padmanabhan, R
/ TITLE: Sequence Analysis of Cloned dengue virus type
/ TITLE: 2 genome (New Guinea-C strain)
/ JOURNAL: Gene
/ VOLUME: 75
/ ISSUE: 2
/ PAGES: 197-211
/ DATE: 1989
/ PUBLICATION INFORMATION:
/ AUTHORS: Yaegashi, T
/ AUTHORS: Vakharia, V N
/ AUTHORS: Page, K
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Feighny, R
/ AUTHORS: Padmanabhan, R
/ JOURNAL: Gene
/ VOLUME: 46
/ ISSUE: 2-3
/ PAGES: 257-267
/ DATE: 1986
/
US-08-869-423-1
Query Match 100.0%; Score 28; DB 4; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 2
US-08-937-195-1
/ Sequence 1, Application US/08937195
/ GENERAL INFORMATION:
/ APPLICANT: IVY, JOHN M.
/ APPLICANT: KAKANO, EILEEN
/ APPLICANT: CLEMENTS, DAVID
/ TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1912
/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/937,195
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: US 08/488,807
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 4733-0003.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2 (Den-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PRI59/S1
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: group(103, 1940, 1991, 2025)
/ OTHER INFORMATION: /note= "Positions in the S1 strain
/ OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain
/ OTHER INFORMATION: reported by Hahn(Citation #1)"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1218
/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1260
/ OTHER INFORMATION: /note= "T is replaced by G for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1762
/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1929
/ OTHER INFORMATION: /note= "C is replaced by T for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2310
/ OTHER INFORMATION: /note= "A is replaced by N for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid."
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
;
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
; US-08-937-195-1
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.00091;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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; Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67
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; RESULT 3
; US-08-937-195-2
; Sequence 2, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
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; US-08-937-195-2
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;

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Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 4
US-08-915-152-1
; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-1

Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 5
US-08-915-152-2
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
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COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: Strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343

OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-915-152-2
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGGCGAGAGAAACCGCG 28
|||||
DB 40 AATATGCTGAAACGGCGAGAGAAACCGCG 67
RESULT 6
PCT-US96-07627-1
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:

NAME/KEY: misc_feature
LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G for
OTHER INFORMATION: Wild-Type sequence"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced by T for
OTHER INFORMATION: Wild-Type sequence"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 2310
OTHER INFORMATION: /note= "A is replaced by N for
OTHER INFORMATION: Wild-Type sequence"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid."

FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"

PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988

PCT-US96-07627-1

Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAACCGCG 28

Db 40 AATATGCTGAACCGAGAGAACCGCG 67

RESULT 7

PCT-US96-07627-2

Sequence 2, Application PC/TUS9607627

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION

NUMBER OF SEQUENCES: 50

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07627
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2(DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PRI59/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PRI5:
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PRI5:
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PRI59
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PRI59
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology

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;
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-2

Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67
|||||

RESULT 8
US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
US-08-325-426B-1

Query Match 94.3%; Score 26.4; DB 3; Length 10718;
Best Local Similarity 96.4%; Pred. No. 0.0063;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 120 AATATGCTGAACGCGAGAGAAACCGCG 147
|||||

RESULT 9
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794

; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Braeh
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annum (green pepper)
US-09-078-173A-11

Query Match 65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 933 AATATGCTGAGATGCAAGAGAAACTGAG 960
|||||

RESULT 10
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-224-391-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
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TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-034-756-5

Query Match 65.7%; Score 18.4; DB 4; Length 12980;
Best Local Similarity 78.6%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
DB 9714 AATATGCTAAACCGCGCATACCCCGCG 9687

RESULT 14
US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60689

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: WHITE LEAF
FEATURE:
NAME/KEY: CDS
LOCATION: 1..657
PUBLICATION INFORMATION:

AUTHORS: Quemada, H
AUTHORS: Kearney, C
AUTHORS: Gonsalves, D
AUTHORS: Slightom, J
TITLE: Nucleotide Sequences of the Coat Protein
Genes and Flanking Regions of Cucumber Mosaic
TITLE: Virus Strains C and WL RNA 3
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
US-08-875-233-11

Query Match 62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGCGAGAGAAACCGCG 28
DB 113 AGATGCTGAACCTCAATAGAACCTCG 139

RESULT 15
US-09-328-352-1888/c
; Sequence 1888, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1888
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 27
DB 964 AATATGCAAAACCGAAGAGAAACCGCG 938

Search completed: August 3, 2004, 19:52:13
Job time : 38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:40:54 ; Search time 158 Seconds
(without alignments)
868.911 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacgcgagagaaacgcgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	14	US-10-085-944-2
2	28	100.0	3381	15	US-10-247-960-2
3	26	92.9	26	9	US-09-840-707A-23
4	26	92.9	26	15	US-10-038-557A-23
5	18.8	67.1	1428	16	US-10-369-493-32952
6	18.6	66.4	1602	15	US-10-156-761-2266
7	18.6	66.4	9025608	15	US-10-156-761-1
8	18.4	65.7	1443	14	US-10-042-991-11
9	18.4	65.7	12980	9	US-09-238-076-5
10	18.4	65.7	12980	10	US-09-995-937-5
11	18.4	65.7	12980	10	US-09-917-563-5
12	18.2	65.0	452	10	US-09-918-995-27460
13	18.2	65.0	2179	13	US-09-823-245A-434
14	18.2	65.0	9875	10	US-09-764-891-7878

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15 17.6 62.9 529 13 US-10-424-599-130933 Sequence 130933,
16 17.6 62.9 550 15 US-10-198-846-11819 Sequence 11819, A
17 17.6 62.9 838 15 US-10-198-846-3468 Sequence 3468, Ap
18 17.6 62.9 945 16 US-10-398-221-2508 Sequence 2508, Ap
19 17.6 62.9 945 16 US-10-398-221-2571 Sequence 2571, Ap
20 17.6 62.9 966 16 US-10-398-221-553 Sequence 553, App
21 17.6 62.9 966 16 US-10-398-221-554 Sequence 554, App
22 17.6 62.9 1646 13 US-10-282-122A-29374 Sequence 29374, A
23 17.6 62.9 9718 8 US-08-319-974A-1 Sequence 1, Appli
24 17.6 62.9 684707 16 US-10-398-221-9 Sequence 9, Appli
25 17.6 62.9 3011208 16 US-10-398-221-2058 Sequence 2058, Ap
26 17.6 62.9 3011208 16 US-10-398-221-2058 Sequence 20, Appl
27 17.4 62.1 379 10 US-09-738-269-20 Sequence 20, Appl
28 17.4 62.1 379 14 US-10-023-437-20 Sequence 20, Appl
29 17.4 62.1 382 17 US-10-437-963-17200 Sequence 17200, A
30 17.4 62.1 528 13 US-10-424-599-53946 Sequence 53946, A
31 17.4 62.1 558 13 US-10-027-632-237136 Sequence 237136,
32 17.4 62.1 558 16 US-10-027-632-237136 Sequence 237136,
33 17.4 62.1 774 13 US-10-282-122A-39862 Sequence 39862, A
34 17.4 62.1 778 13 US-10-282-122A-36749 Sequence 36749, A
35 17.4 62.1 983 14 US-10-011-033-11 GENERAL INFORMA
36 17.4 62.1 2520 10 US-09-738-269-22 Sequence 22, Appl
37 17.4 62.1 2520 14 US-10-023-437-22 Sequence 22, Appl
38 17.4 62.1 2646 13 US-10-194-163-558 Sequence 558, App
39 17.4 62.1 2784 17 US-10-437-963-21921 Sequence 21921, A
40 17.4 62.1 5026 15 US-10-371-101-3 Sequence 3, Appli
41 17.4 62.1 6612 15 US-10-371-101-5 Sequence 5, Appli
42 17.4 62.1 11207 15 US-10-371-101-2 Sequence 2, Appli
43 17.4 62.1 39726 15 US-10-309-933-1 Sequence 1, Appli
44 17.4 62.1 145068 17 US-10-322-281-33 Sequence 33, Appl
45 17.4 62.1 235070 13 US-10-087-192-1990 Sequence 1990, Ap

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ALIGNMENTS

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RESULT 1
US-10-085-944-2
; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

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Query Match 100.0%; Score 28; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |

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RESULT 2
US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.

```

; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-2005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match 100.0%; Score 28; DB 15; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCGCG 28
|||||
DB 40 AATATGCTGAAACCGCGAGAGAAACCGCG 67
|||||

RESULT 3

US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US20020077261A
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-09-840-707A-23

Query Match 92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||
DB 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||

RESULT 4

US-10-038-557A-23
; Sequence 23, Application US/10038557A

; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match 92.9%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||
DB 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||

RESULT 5

US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 16; Length 1428;
Best Local Similarity 90.9%; Pred. No. 1.1e+02; Mismatches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAAACCGCGAGAGAAACCGCG 28
|||||
DB 1184 CGGAACCGCGAGAGAAACCGCG 1163
|||||

RESULT 6

US-10-156-761-2266
; Sequence 2266, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:


```

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2266
; TYPE: DNA
; LENGTH: 1602
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2266

Query Match      66.4%; Score 18.6; DB 15; Length 1602;
Best Local Similarity 84.0%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGACCGCGAGAGAACCGCG 28
Db 115 AAGCTGACCGCGAGAGAACCGCG 139

RESULT 7
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      66.4%; Score 18.6; DB 15; Length 9025608;
Best Local Similarity 84.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGACCGCGAGAGAACCGCG 28
Db 2778649 AAGCTGACCGCGAGAGAACCGCG 2778625
```

```

RESULT 8
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUJAVIA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.000103
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match      65.7%; Score 18.4; DB 14; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAACCGCG 28
Db 933 AAATGCTGAGATGCAAGAGAACTGAG 960

RESULT 9
US-09-238-076-5/c
; Sequence 5, Application US/09238076
; Patent No. US20020102540A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-238-076-5
Query Match 65.7%; Score 18.4; DB 9; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 6;
Qy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACCGCGCATACCCCGCG 9687

RESULT 10
US-09-995-937-5/c
; Sequence 5, Application US/09995937
; Publication No. US20030028010A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,563
; FILING DATE: 27-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/238,076
; FILING DATE: 26-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5
Query Match 65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 6;
Qy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACCGCGCATACCCCGCG 9687

RESULT 12
US-09-918-995-27460
; Sequence 27460, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27460
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
```


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:26:44 ; Search time 1253 Seconds
(without alignments)
667.311 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacgcgagagaacgcg 28

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.6	73.6	776	14	CF996467
2	19.8	70.7	720	14	CF455745
3	19.6	70.0	301	14	CB078143
4	19.6	70.0	712	14	CF372439

C	5	19.6	70.0	722	14	CF512147
C	6	19.6	70.0	734	14	CF512236
C	7	19.4	69.3	464	10	BE841207
C	8	19	67.9	559	29	TA262H01Q
C	9	19	67.9	568	28	AQ945692
C	10	19	67.9	576	29	TA140D12P
C	11	19	67.9	580	10	BE776235
C	12	19	67.9	602	9	AL673619
C	13	19	67.9	629	9	AL674632
C	14	19	67.9	633	14	CA349616
C	15	19	67.9	649	14	CA356841
C	16	19	67.9	768	29	CC504335
C	17	19	67.9	768	29	AG186531
C	18	19	67.9	870	29	AG186531
C	19	18.8	67.1	1687	10	CF995511
C	20	18.6	66.4	407	14	CF198531
C	21	18.6	66.4	456	12	BG659286
C	22	18.6	66.4	563	14	CF93381
C	23	18.6	66.4	584	28	AQ657703
C	24	18.6	66.4	593	29	FR0021761
C	25	18.6	66.4	642	9	AI135620
C	26	18.6	66.4	684	28	AQ657387
C	27	18.4	65.7	427	29	CG016439
C	28	18.4	65.7	456	28	AQ724090
C	29	18.4	65.7	496	10	AW592272
C	30	18.4	65.7	582	28	B2130571
C	31	18.4	65.7	655	14	CB020289
C	32	18.4	65.7	672	28	BH100535
C	33	18.4	65.7	675	13	CA112278
C	34	18.4	65.7	695	28	BH929269
C	35	18.4	65.7	697	28	BH549312
C	36	18.4	65.7	743	14	CK326303
C	37	18.4	65.7	750	10	BE615972
C	38	18.4	65.7	774	28	B2154086
C	39	18.4	65.7	788	28	B2132164
C	40	18.4	65.7	790	10	BF678988
C	41	18.4	65.7	792	12	BI753870
C	42	18.4	65.7	824	10	BF620613
C	43	18.4	65.7	1101	29	CNS00KGJ
C	44	18.4	65.7	1126	9	AL697344
C	45	18.4	65.7	1253	10	BF690226

ALIGNMENTS

RESULT 1
CF996467/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF996467
AGENCOURT_16394292 NIH_ZGC_7
5', mRNA sequence.
CF996467
CF996467.1 GI:38517318
EST:
Danio rerio (zebrafish)
Danio rerio
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteiophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 776)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LAM14788 row: e column: 03
 High quality sequence stop: 734.

FEATURES

source
 1. .776
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7037741"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC 7"
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments and
 normalized. A non-normalized version of this library is
 also available (NIH_ZGC10). Library was constructed by
 Open Biosystems (Huntsville, AL)"

Query Match 73.6%; Score 20.6; DB 14; Length 776;
 Best Local Similarity 85.2%; Pred. No. 1.7e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGGAGAGAAACCGCG 28
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 549 ATGTGCTGACACGCGAGAGACCGAG 523

RESULT 2
 CF455745
 LOCUS
 DEFINITION
 AGENCOURT 15376947 Human Anterior Horn Homo sapiens cDNA clone
 IMAGE:30515857 5', mRNA sequence.
 CF455745
 CF455745.1 GI:34455401
 EST.
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 720)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: gcgbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM581 row: k column: 02
 High quality sequence start: 194
 High quality sequence stop: 544.

source
 1. .720
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30515857"
 /tissue_type="Peripheral Nervous system"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="Human Anterior Horn"

ORIGIN

Query Match 70.7%; Score 19.8; DB 14; Length 720;
 Best Local Similarity 91.3%; Pred. No. 3.7e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAA 23
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 189 AAGATGCTGAACACCGAGAGAAA 211

RESULT 3
 CB078143
 LOCUS
 DEFINITION
 h363h04.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
 terminalis cDNA clone h363h04, mRNA sequence.
 CB078143
 CB078143.1 GI:27891580
 EST.
 Hedyotis terminalis
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Gentianales; Rubiaceae; Rubioloideae;
 Spermacoceae; Hedyotis.
 1 (bases 1 to 301)
 Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
 O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
 Bentley,P. and Stevenson,D.
 Expressed tag sequences from Hedyotis terminalis flower - Stage 2
 (NYBG)

FEATURES

source
 1. .301
 /organism="Hedyotis terminalis"
 /mol_type="mRNA"
 /db_xref="taxon:219667"
 /clone="h363h04"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
 /notes="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Strategene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2562"

Query Match 70.0%; Score 19.6; DB 14; Length 301;
 Best Local Similarity 84.8%; Pred. No. 3.6e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACCGGAGAGAAACCGCG 28
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 212 TATGCTGAACGTGACAGAGCGCG 237

RESULT 4

ORIGIN

Query Match 70.0%; Score 19.6; DB 14; Length 301;
 Best Local Similarity 84.8%; Pred. No. 3.6e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACCGGAGAGAAACCGCG 28
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 212 TATGCTGAACGTGACAGAGCGCG 237

RESULT 4

Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers

```

1..722
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon (Clone 8)"
/db_xref="taxon:29760"
/clone="CABUD003 IF_A10"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom (10-11 days before bloom)"
/lab_host="DH5alpha"
/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"
/note="Organ Bud; Vector: pDNR; Site 1: SfilI; Site 2: SfilI; CABUD is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCATGCTATCACGAGTGCCATTACGGCCGG-3' and
5'-ATTCTAGACGGCGGCAGCATG-TT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

```

ORIGIN

Query Match	70.0%; Score 19.6; DB 14; Length 722;
Best Local Similarity	84.6%; Pred. No. 4.5e+02;
Matches	22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1  ATATGCTGAACGCGGAGNAACCG 26
          ||||| ||||| ||||| ||||| |||||
DB     350 ACTATGCTGAACACTCGAAGAACA CTG 325

```

RESULT 6

CF512236 linear EST 09-SEP-2003

LOCUS
CABud0003_IR_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone CABud0003_IR_A10 3', mRNA sequence.

VERSION
CF512236.1 GI:34544004

KEYWORDS
EST.

ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolo,A., Lim,H., Baek,J., Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
Unpublished (2003)

JOURNAL COMMENT
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: GCCAACGAATGCTTAG.

VERSION	AL466434.1	GI:11835789
KEYWORDS	GSS.	
SOURCE	Trypanosoma brucei	
ORGANISM	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	
REFERENCE	1 (bases 1 to 576)	
AUTHORS	Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A. and Barrell, B. G.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk	
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	
FEATURES	Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.	
source	Location/Qualifiers	
	1..576	
	/organism="Trypanosoma brucei"	
	/mol_type="genomic DNA"	
	/strain="TREU927"	
	/db_xref="taxon:5691"	
	/clone="140d12"	
ORIGIN		
Query Match	67.9%;	Score 19; DB 29; Length 576;
Best Local Similarity	81.5%;	Pred. No. 7.9e+02;
Matches	22; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	2 ATATGCTGAACGCGAGAGAACCGCG 28	
Db	231 ATATGCAGAAACGCGAGCAAGGACG 257	
RESULT 11		
BE776235		
LOCUS	BE776235	580 bp mRNA linear EST 20-SEP-2000
DEFINITION	MY-12-F-04 PinfeastanMY Phytophthora infestans cDNA, mRNA sequence.	
ACCESSION	BE776235	
VERSION	BE776235.1	GI:10229890
KEYWORDS	EST.	
SOURCE	Phytophthora infestans (potato late blight agent)	
ORGANISM	Phytophthora infestans	
	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.	
REFERENCE	1 (bases 1 to 580)	
AUTHORS	Kamoun, S., Hraber, P. T., Sobral, B. W. S., Nuss, D. and Govers, F.	
TITLE	Initial assessment of gene diversity for the oomycete pathogen Phytophthora infestans based on expressed sequences	
JOURNAL	Fungal Genet. Biol. 28 (2): 94-106 (1999)	
MEDLINE	20056376	
PUBMED	10587472	
COMMENT	Contact: Govers F Laboratory of Phytopathology Wageningen University Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands Tel: 31 317 483 138 Fax: 31 317 483 412 Email: Francine.Govers@medew.fyto.wau.nl.	
FEATURES	Location/Qualifiers	
source	1..580	
	/organism="Phytophthora infestans"	

/mol_type="mRNA"
 /strain="DDR7602, A1 mating type"
 /db_xref="taxon:4787"
 /dev_stage="4-week old vegetative, non-sporulating
 mycelium in synthetic medium"
 /lab_host="E. coli, strain DHS-alpha"
 /clone_lib="PinfestansMY"
 /notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Total
 RNA was isolated from mycelium of P. infestans DDR7602
 cultured for 4 weeks in synthetic medium. EST clones were
 named by their position in the microtiter plate, preceded
 by the prefix MY (for mycelial) and the successive number
 of the microtiter plate (e.g. MY-06-A-04)."

ORIGIN

Query Match 67.9%; Score 19; DB 10; Length 580;
 Best Local Similarity 81.5%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCGCG 28

Db 325 ATGAGCTGATACGCGAGAGAACCGCG 351

RESULT 12
 LOCUS AL673619 602 bp mRNA linear EST 10-NOV-2003
 DEFINITION AL673619 XGC-neurula Silurana tropicalis cDNA clone TNeu062m06 5',
 mRNA sequence.

ACCESSION AL673619

VERSION

KEYWORDS

SOURCE

ORGANISM

Silurana tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Silurana.

REFERENCE
 1 (bases 1 to 602)
 Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT On Mar 18, 2002 this sequence version replaced gi:19529975.

CONTACT: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

cDNA was oligo dt primed from Sug of poly A+ RNA from neurula.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli DH10B

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TNeu062m06.plcSP6

Sequencing primer: SP6.

FEATURES

source

1..602

/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TNeu062m06"

/dev_stage="neurula"

/lab_host="Escherichia coli DH10B"

/clone_lib="XGC-neurula"

/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from Sug of poly A+ RNA from neurula.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 602;
 Best Local Similarity 81.5%; Pred. No. 8e+02;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCGCG 28

Db 202 ATAAGCTGAAGCGCGAGAGAACGTG 228

RESULT 13

LOCUS AL647632

DEFINITION AL647632 XGC-gastrula Silurana tropicalis cDNA clone TGas037f09 5',
 mRNA sequence.

ACCESSION AL647632

VERSION

KEYWORDS

SOURCE

ORGANISM

Silurana tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Silurana.

REFERENCE
 1 (bases 1 to 629)

Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT On Dec 13, 2001 this sequence version replaced gi:17655942.

CONTACT: Huckle E
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

cDNA was oligo dt primed from Sug of poly A+ RNA from stages 10-13
 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli XLI-blue

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TGas037f09.plkSP6

Sequencing primer: SP6.

FEATURES

source

1..629

/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TGas037f09"

/dev_stage="gastrula (stages 10.5-12 mixed)"

/lab_host="Escherichia coli XLI-blue"

/clone_lib="XGC-gastrula"

/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from Sug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 629;

Best Local Similarity 81.5%; Pred. No. 8.1e+02;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCGCG 28

Db 234 ATAAGCTGAAGCGCGAGAGAACGTG 260

RESULT 14

LOCUS CA349616

DEFINITION CA349616 633 bp mRNA linear EST 05-NOV-2002
 620082 NCCOWA 1RT Oncorhynchus mykiss cDNA clone 1RT142M04_C_G02
 5', mRNA sequence.

ACCESSION CA349616

VERSION

KEYWORDS

SOURCE

Oncorhynchus mykiss (rainbow trout)

ORGANISM

Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

1 (bases 1 to 633)
Rexroad,C.E. and Keele,J.W.
Sequence analysis of a rainbow trout normalized cDNA library
Unpublished (2002)

AUTHORS

Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351

JOURNAL

Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.

COMMENT

Seq primer: AGCGGATACAAATTCACACAGGA.

FEATURES

source

Location/Qualifiers
1..633

/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="IRT142M04_C_G02"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN

Query Match

Best Local Similarity 81.5%; Score 19; DB 14; Length 633;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY

1 AATATGCTGAAACGCGAGAGAAACCGC 27

||||| ||| ||||| ||| |||

Db

579 AATATGCAGAACTGCGAGAGAGCTGC 605

RESULT 15

CA356841

LOCUS

629106 NCCCWA 1RT Oncorhynchus mykiss cDNA clone IRT100M13_A_G07
5', mRNA sequence.

DEFINITION

CA356841

CA356841.1 GI:24602028

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oncorhynchus mykiss (rainbow trout)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 649)

Rexroad,C.E. and Keele,J.W.

Sequence analysis of a rainbow trout normalized cDNA library

Unpublished (2002)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA

Tel: 304 724 8340 x2129

Fax: 304 725 0351

Email: crexroad@nccwa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified by

cross_match v0.990329.

Seq primer: AGCGGATACAAATTCACACAGGA.

Location/Qualifiers

1..649

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

ORIGIN

Query Match

Best Local Similarity 81.5%; Score 19; DB 14; Length 649;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY

1 AATATGCTGAAACGCGAGAGAAACCGC 27

||||| ||| ||||| ||| |||

Db

469 AATATGCAGAACTGCGAGAGAGCTGC 495

Search completed: August 3, 2004, 19:50:58

Job time : 1257 secs

/clone="IRT100M13_A_G07"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

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